US008399622B2

(12) **United States Patent**
Ring et al.

(10) **Patent No.: US 8,399,622 B2**
(45) **Date of Patent: Mar. 19, 2013**

(54) **REAGENTS AND METHODS FOR USE IN CANCER DIAGNOSIS, CLASSIFICATION AND THERAPY**

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(*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 0 days.

(21) Appl. No.: **13/300,134**

(22) Filed: **Nov. 18, 2011**

(65) **Prior Publication Data**

US 2012/0065107 A1 Mar. 15, 2012

Related U.S. Application Data

(60) Division of application No. 12/879,356, filed on Sep. 10, 2010, which is a division of application No. 12/013,739, filed on Jan. 14, 2008, now Pat. No. 7,811,774, which is a division of application No. 11/061,067, filed on Feb. 18, 2005, now abandoned, which is a continuation-in-part of application No. 10/915,059, filed on Aug. 10, 2004, now abandoned.

(60) Provisional application No. 60/494,334, filed on Aug. 11, 2003, provisional application No. 60/570,206, filed on May 12, 2004.

(51) **Int. Cl.**
C07K 16/00 (2006.01)

(52) **U.S. Cl.** **530/387.1**; 530/387.7

(58) **Field of Classification Search** ..... None
See application file for complete search history.

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(57) **ABSTRACT**

Methods and reagents for classifying tumors and for identifying new tumor classes and subclasses. Methods for correlating tumor class or subclass with therapeutic regimen or outcome, for identifying appropriate (new or known) therapies for particular classes or subclasses, and for predicting outcomes based on class or subclass. New therapeutic agents and methods for the treatment of cancer.

15 Claims, 13 Drawing Sheets

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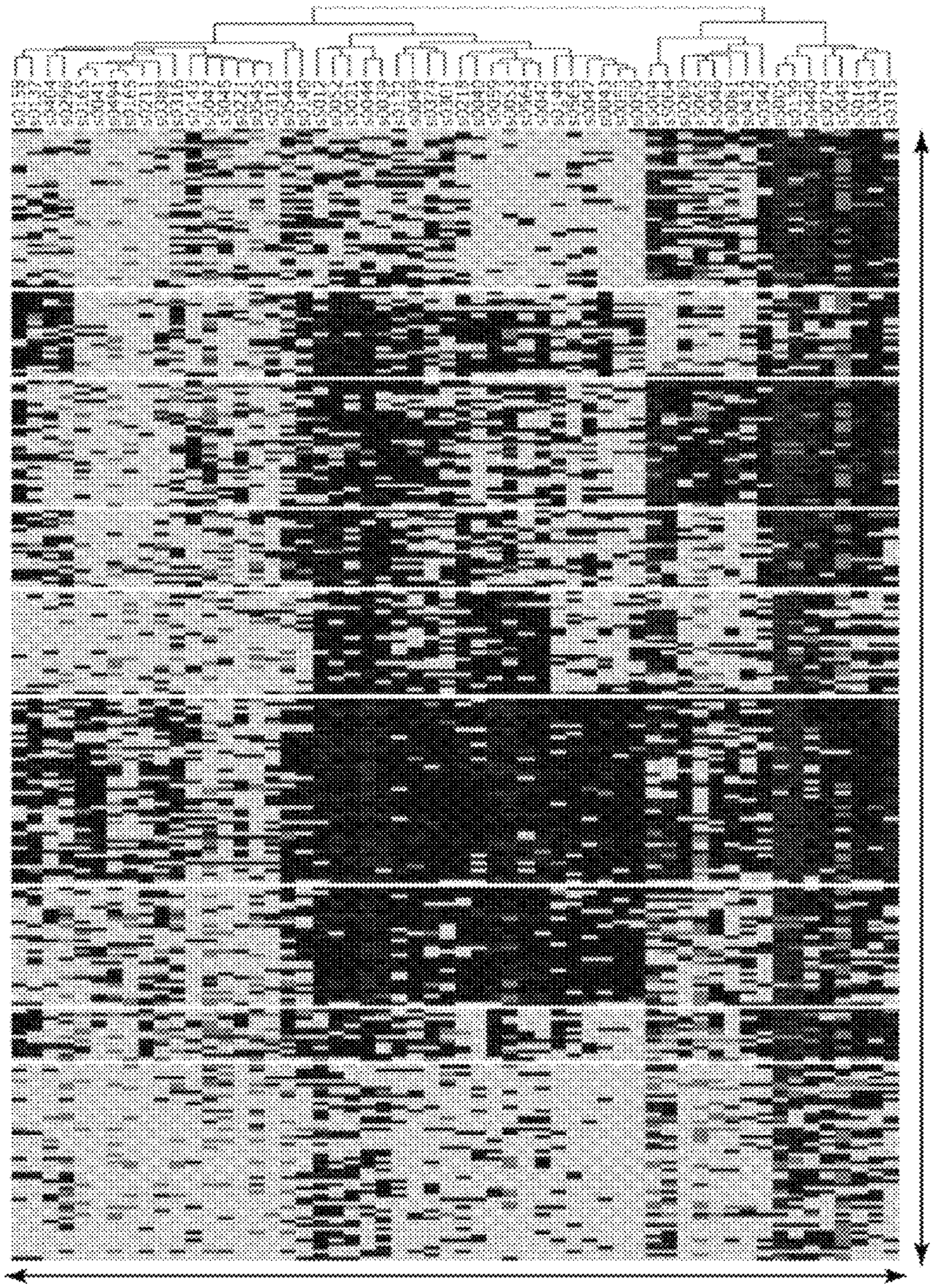


FIG. 1

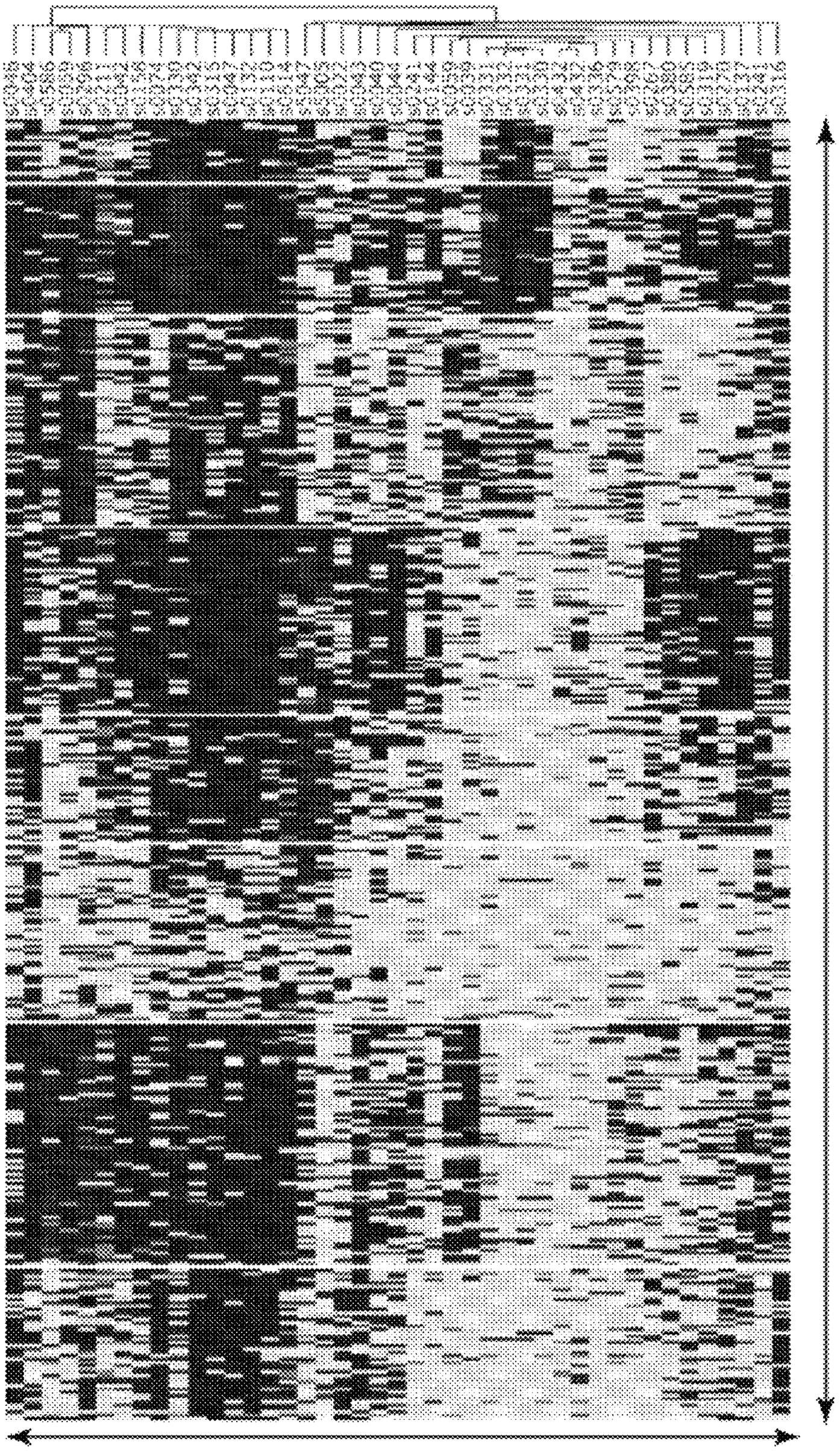


FIG. 2

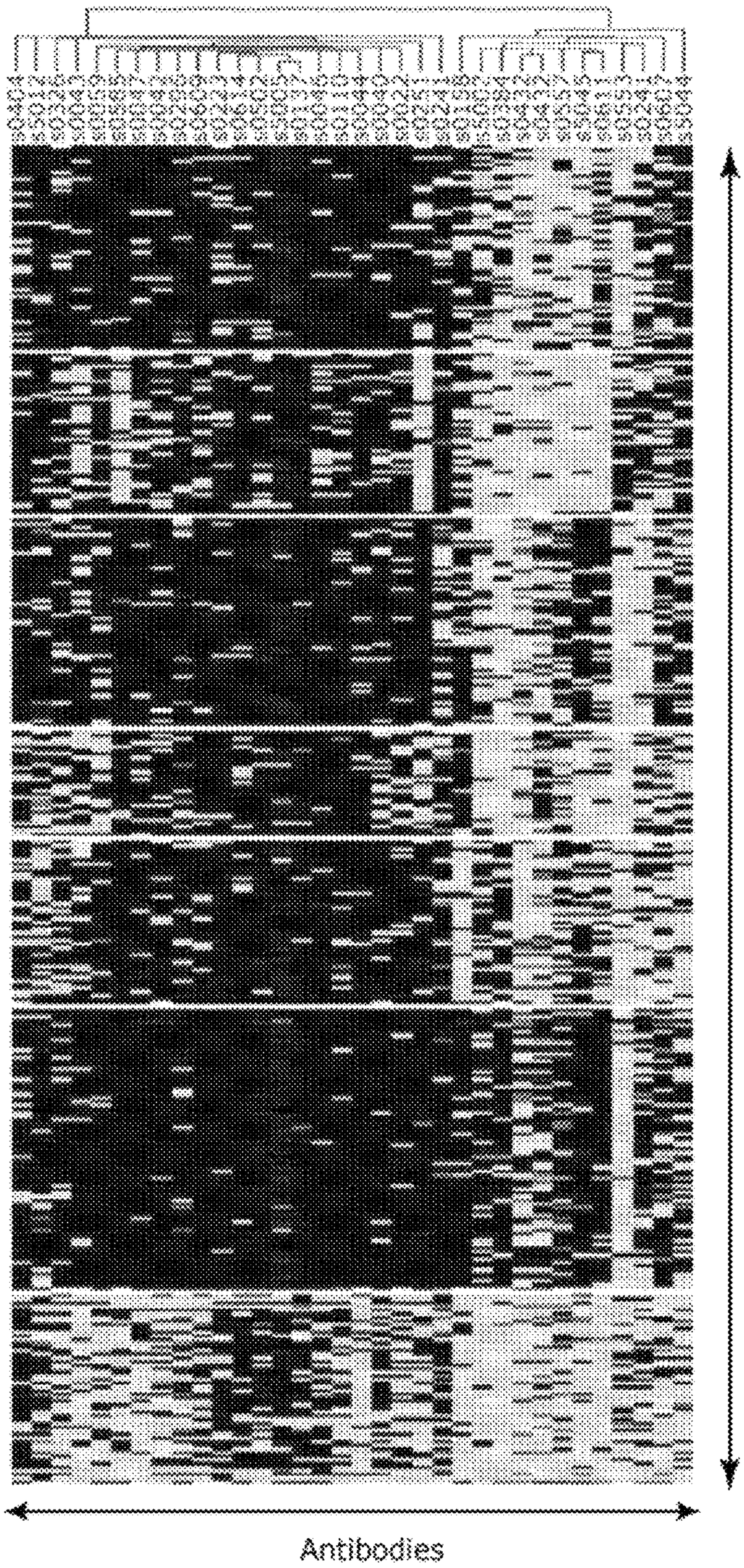


FIG. 3

Figure 4A

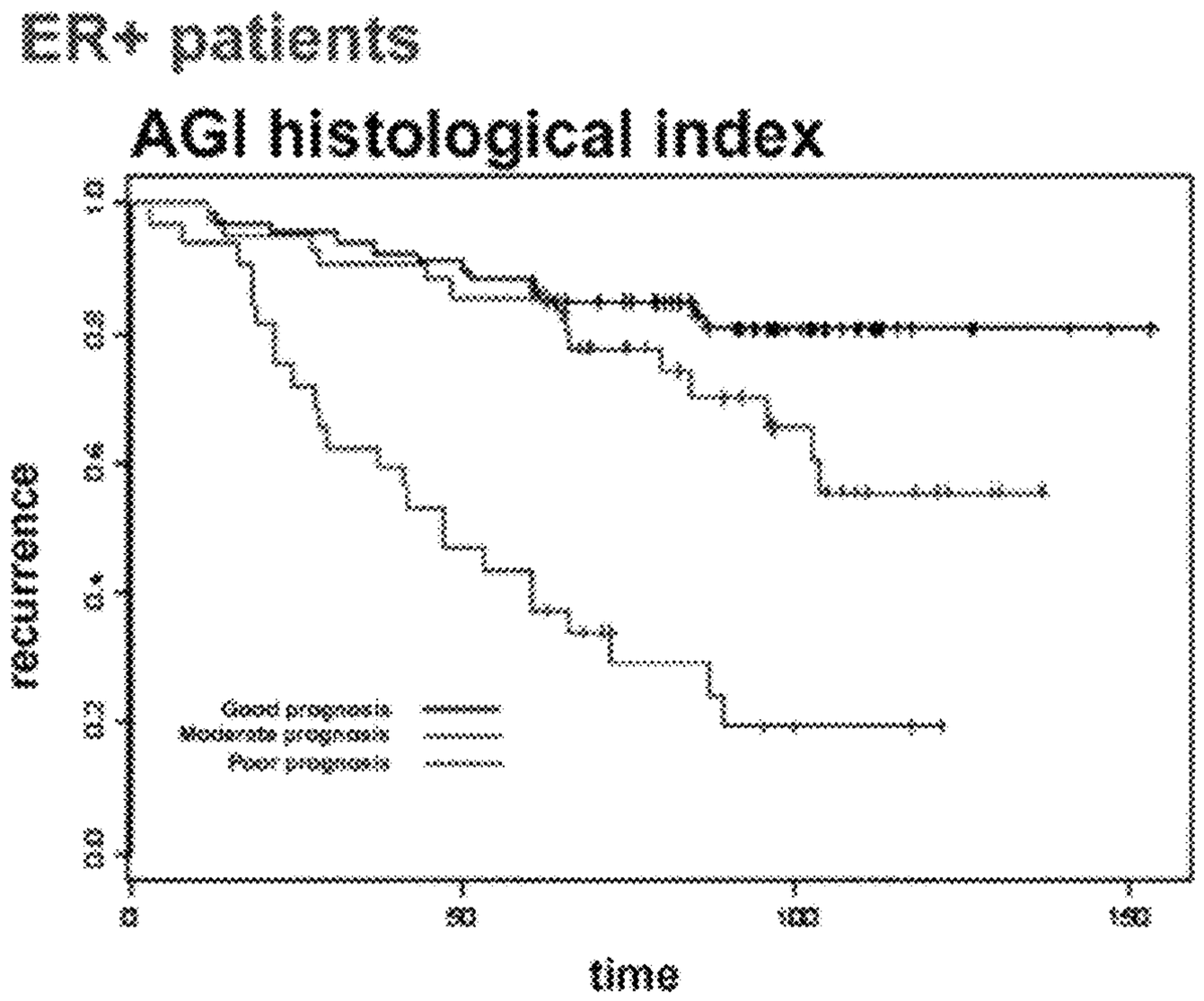


Figure 4B

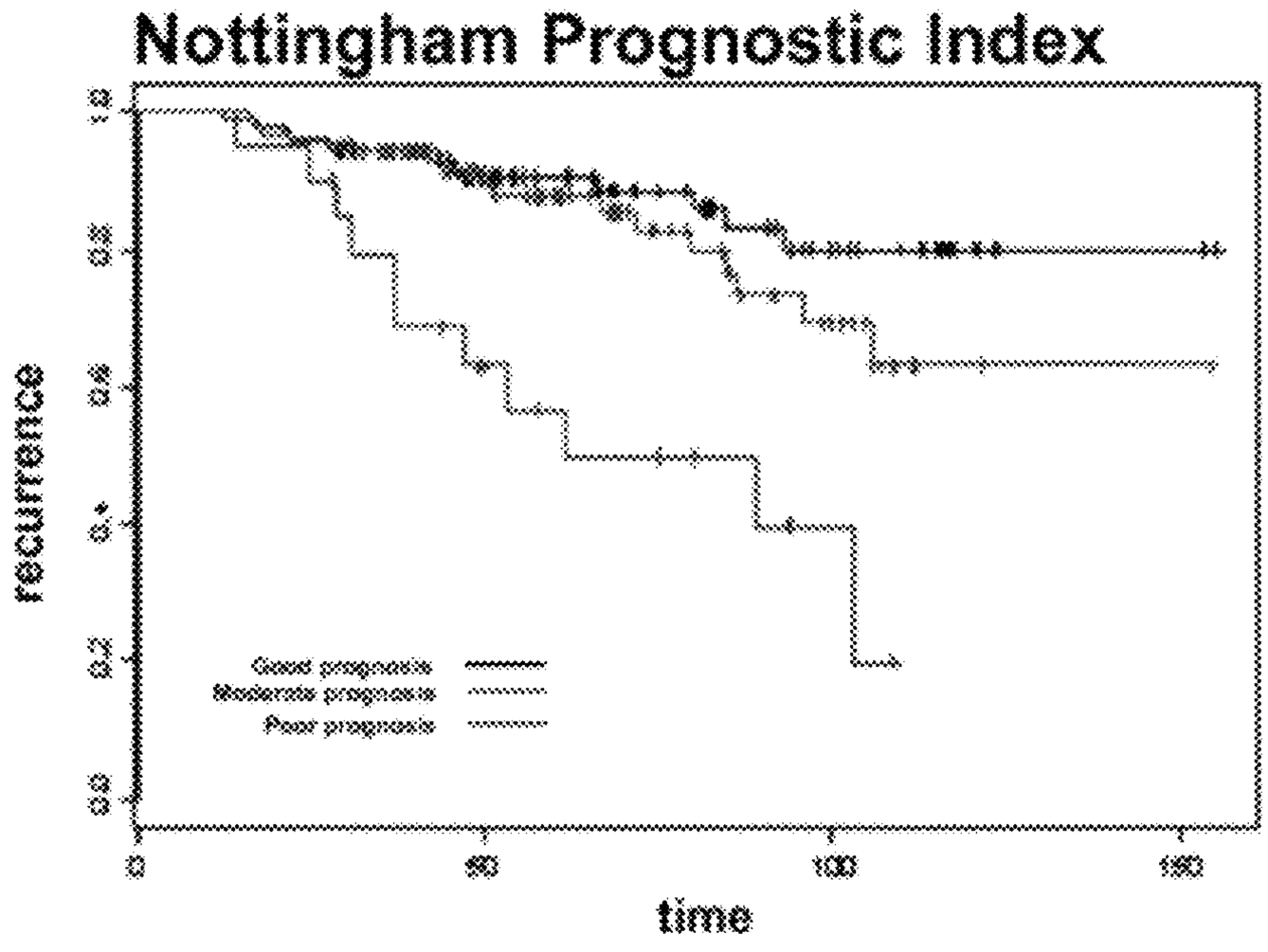


Figure 5A

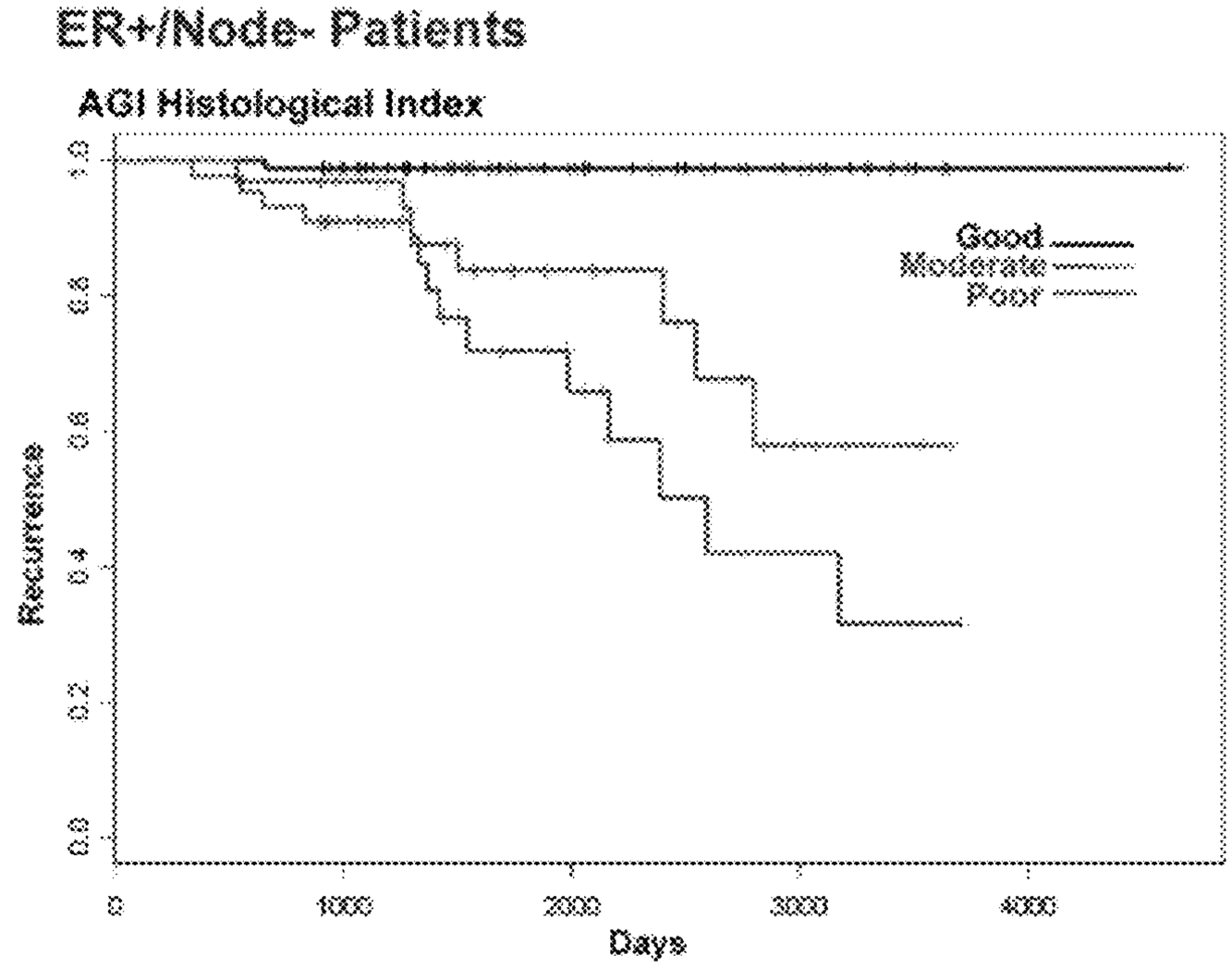
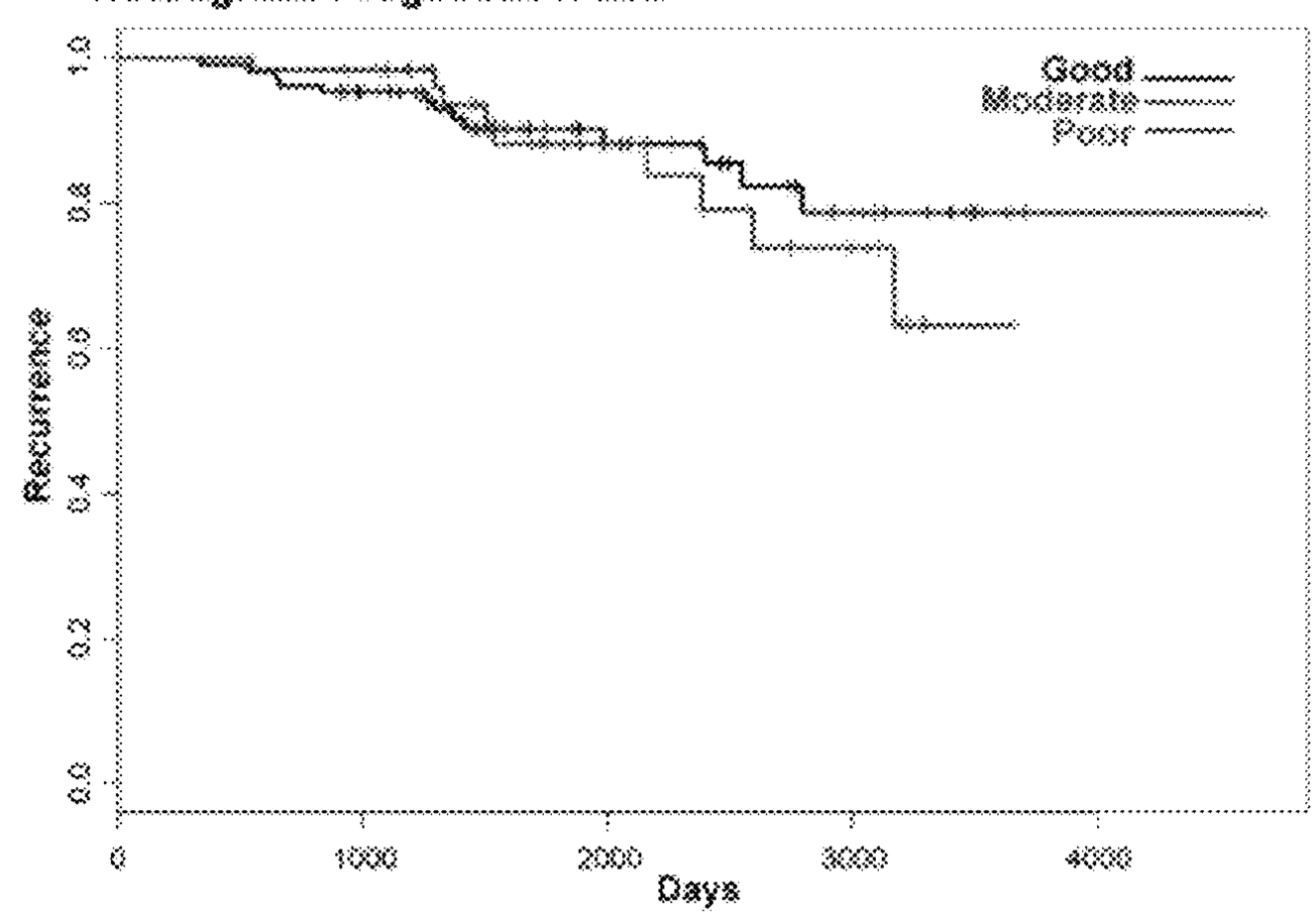


Figure 5B



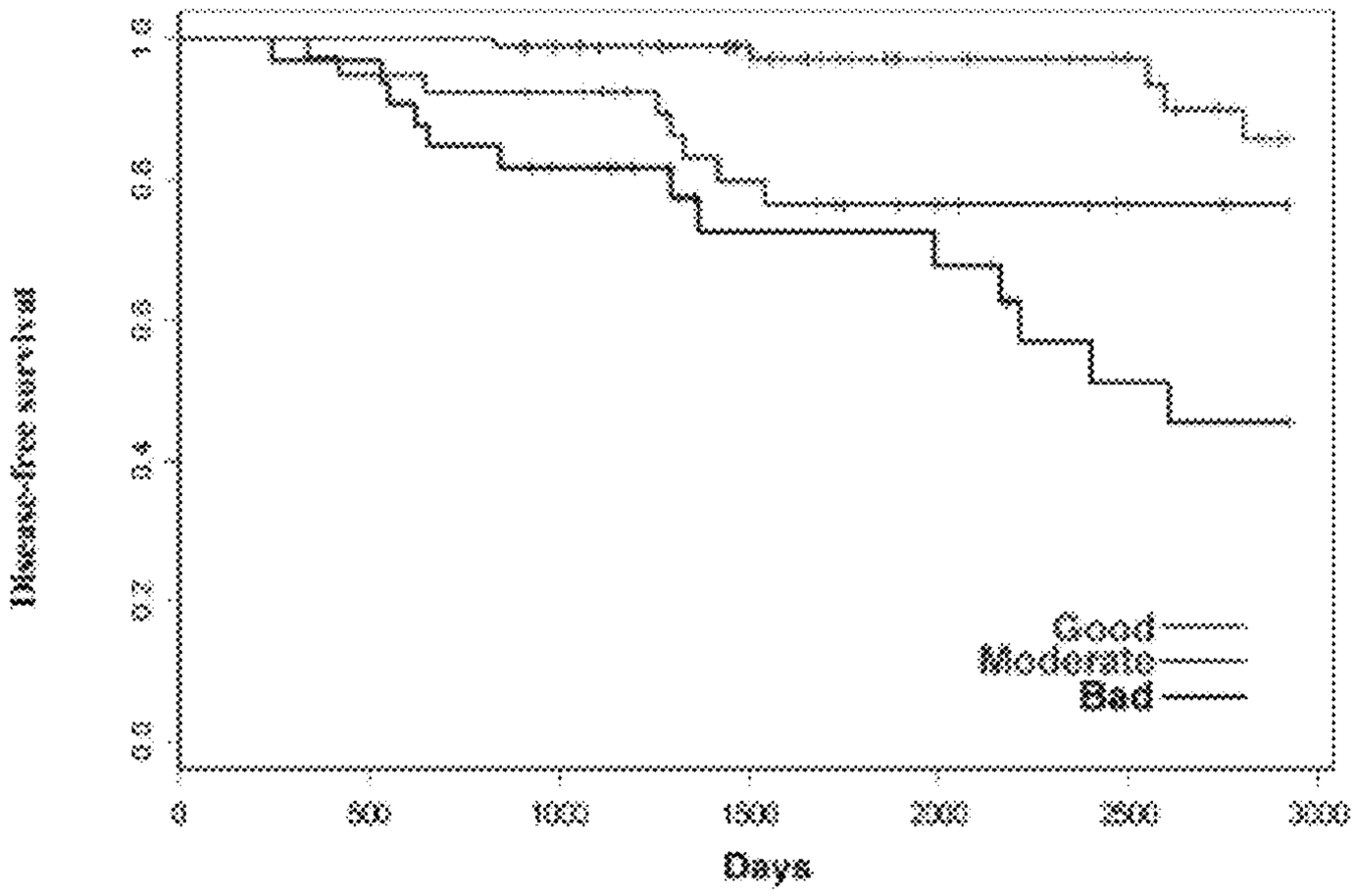


Figure 6

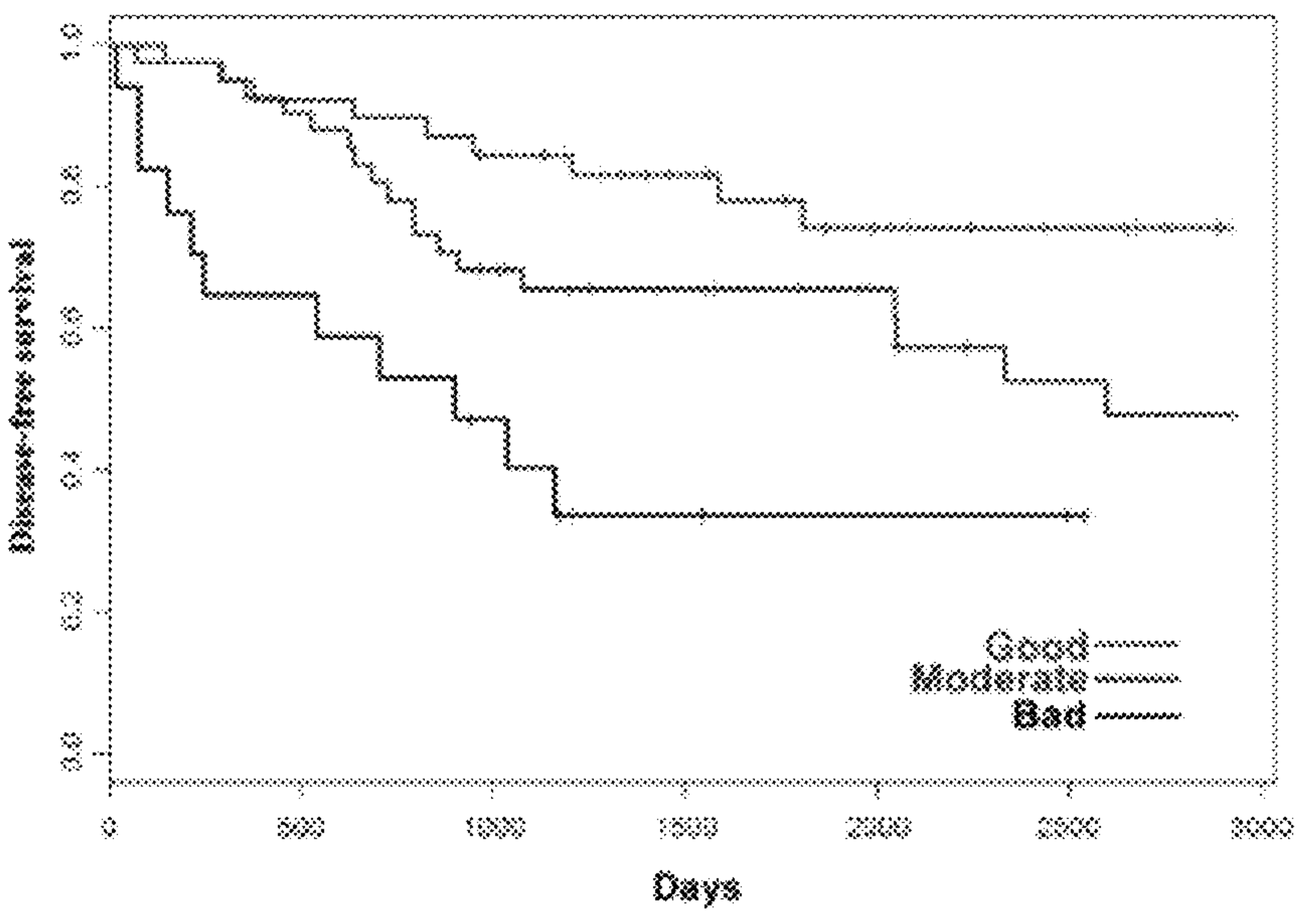


Figure 7

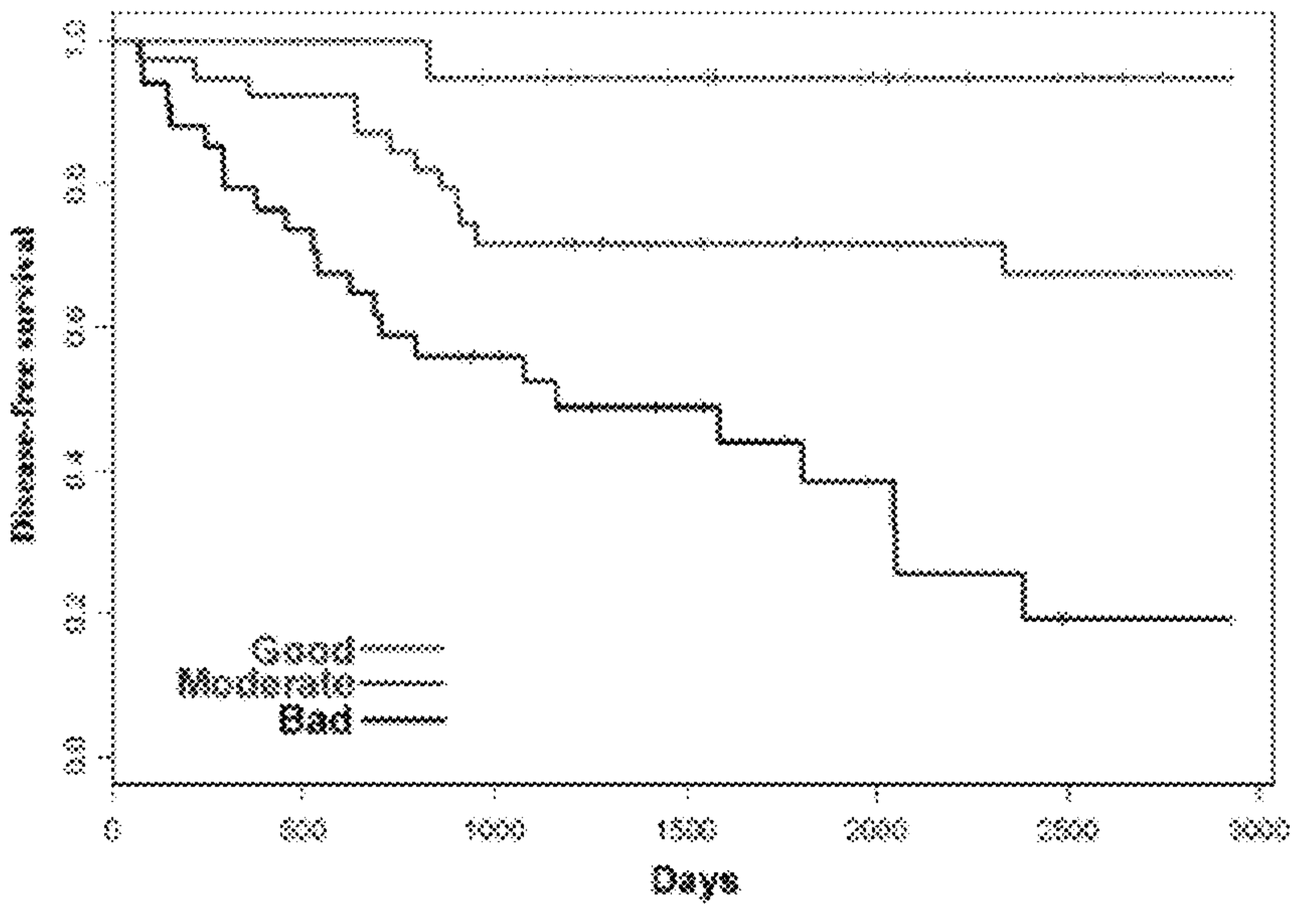


FIGURE 8

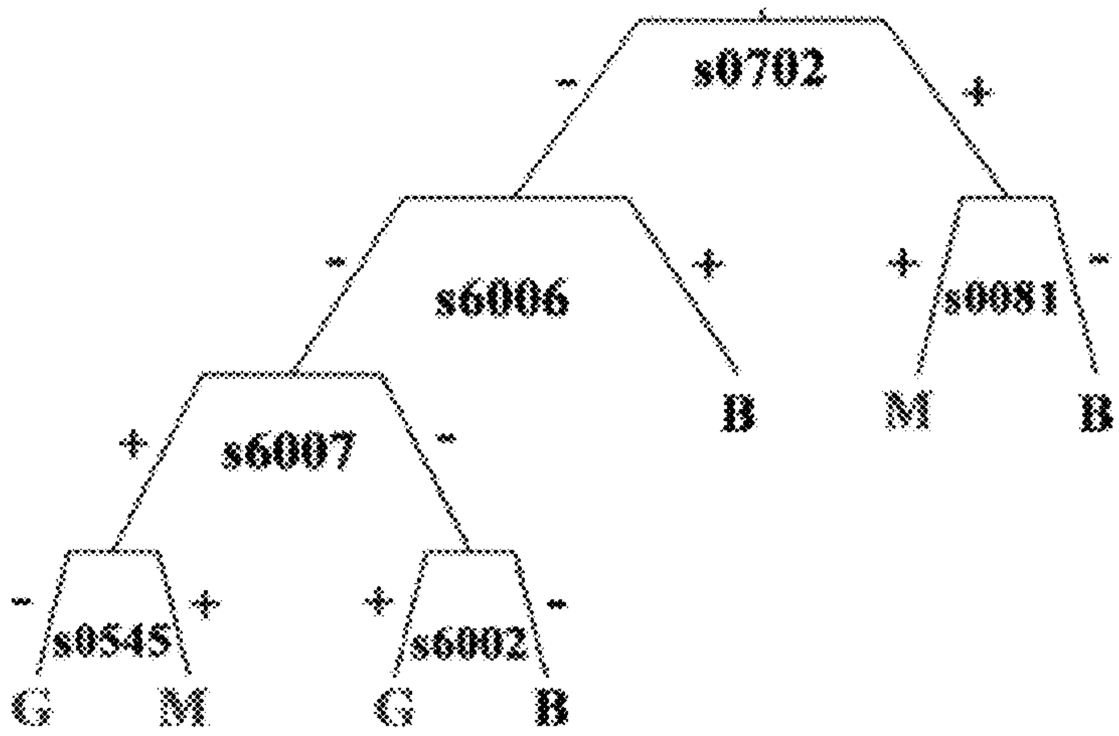


FIGURE 9

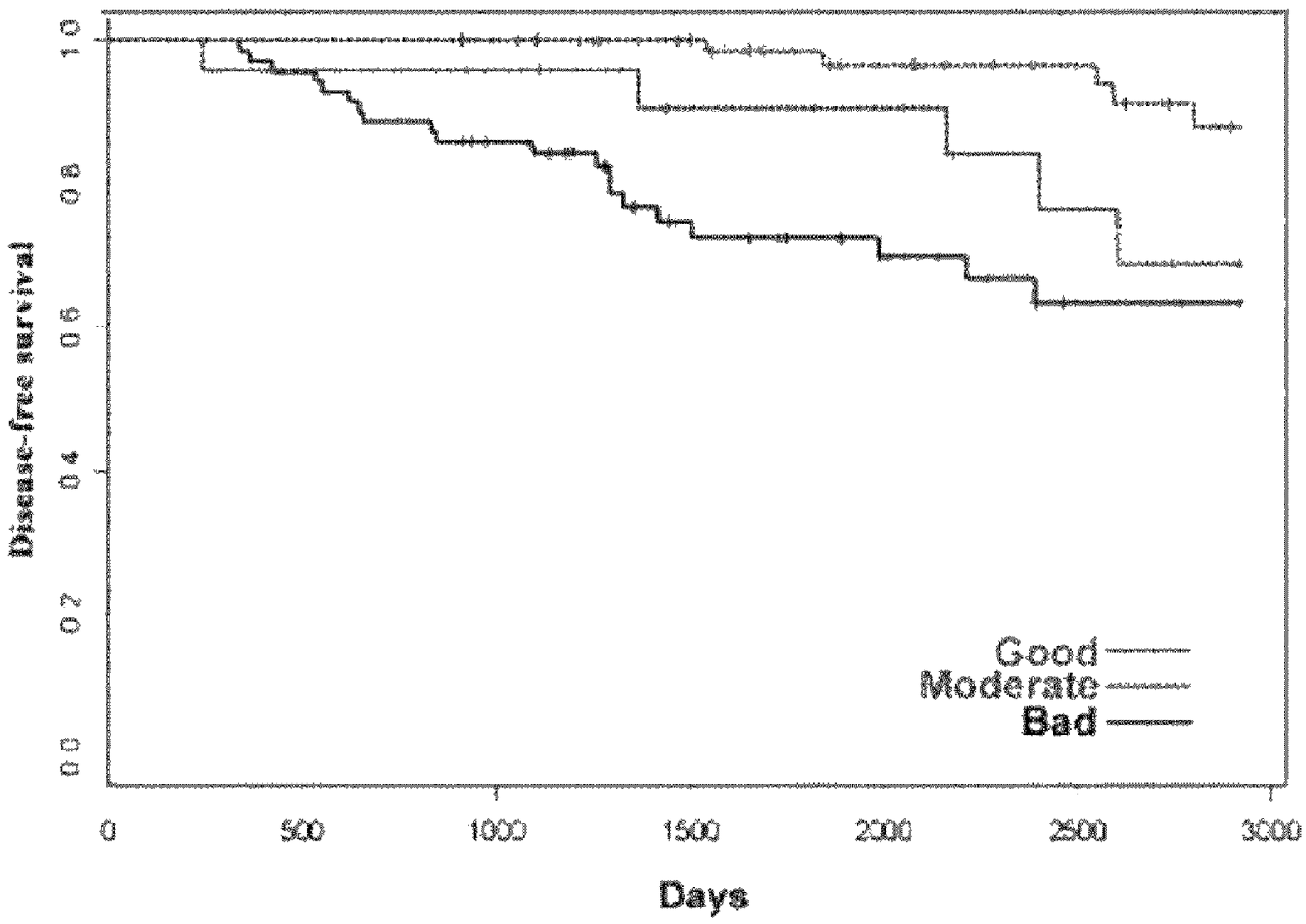
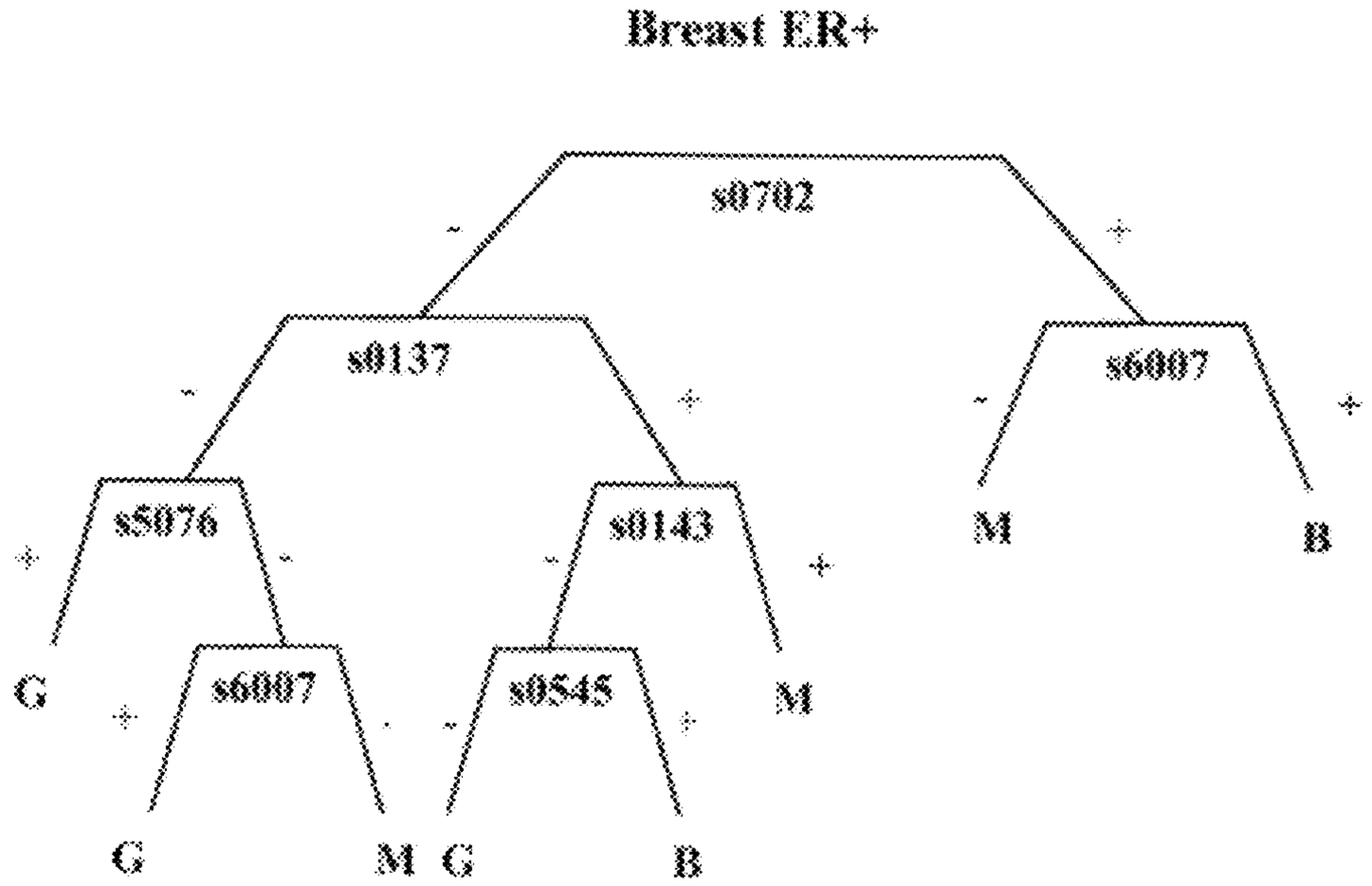

Disease-free survival
1.0
0.8
0.6
0.4
0.2
0.0
0
500
1000
1500
2000
2500
3000
Days
Good
Moderate
Bad

FIGURE 10


Breast ER+
s0702
s0137
s6007
s5076
s0143
M
B
G
s6007
s0545
M
G
M
G
B

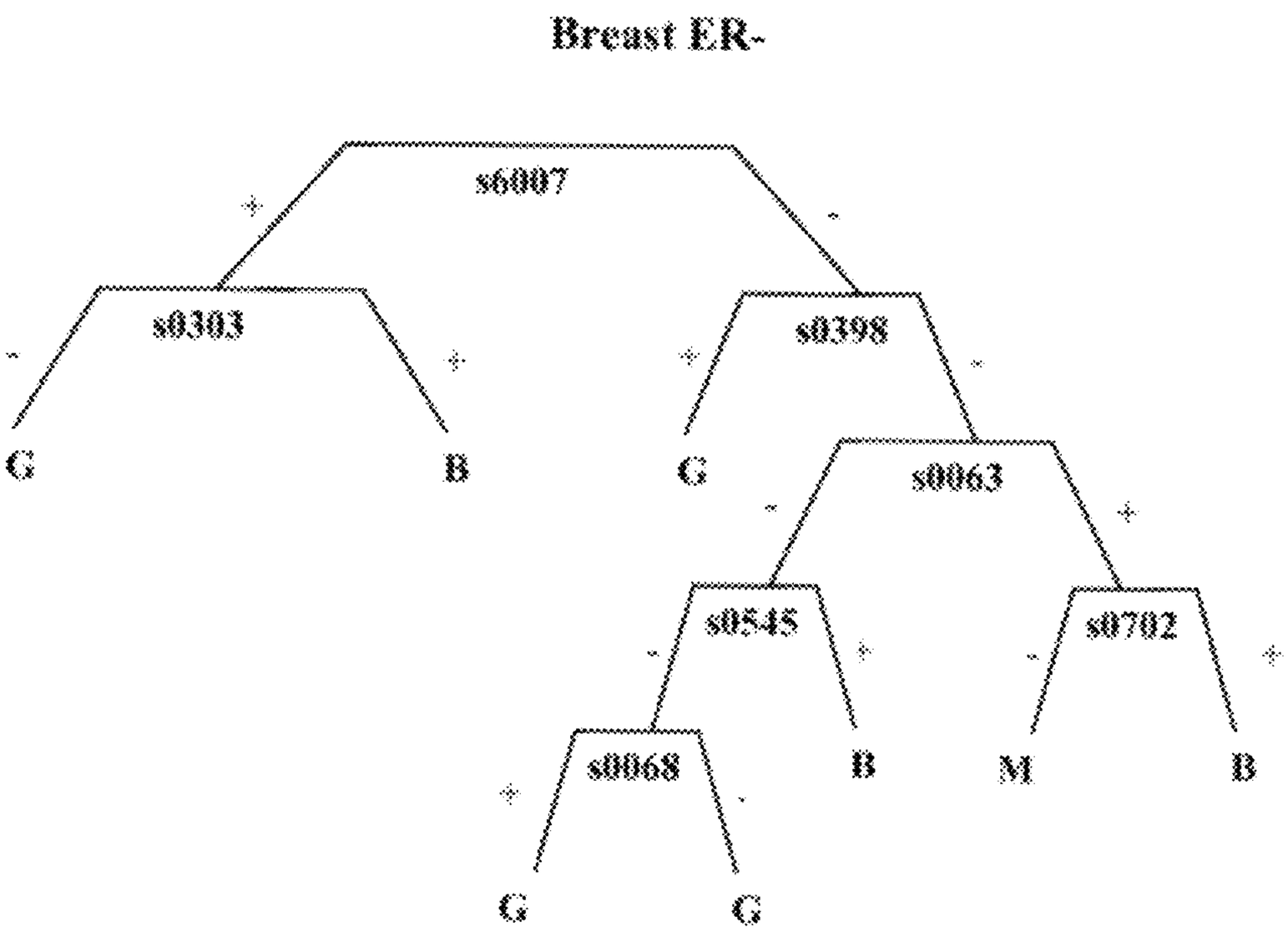

Breast ER-
s6007
s0303
s0398
G
B
G
s0063
s0545
s0702
s0068
B
M
B
G
G

FIGURE 11

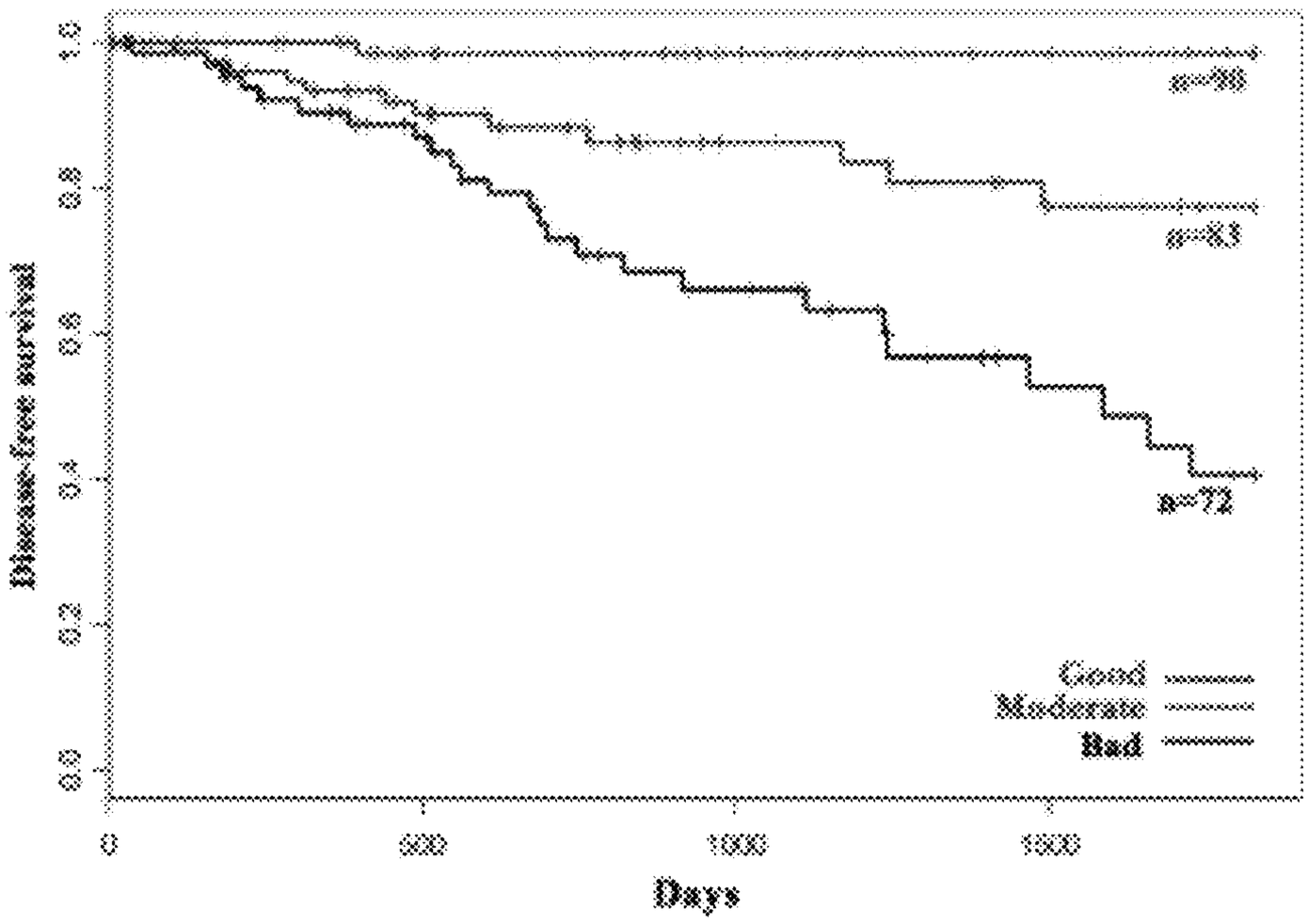


FIGURE 12

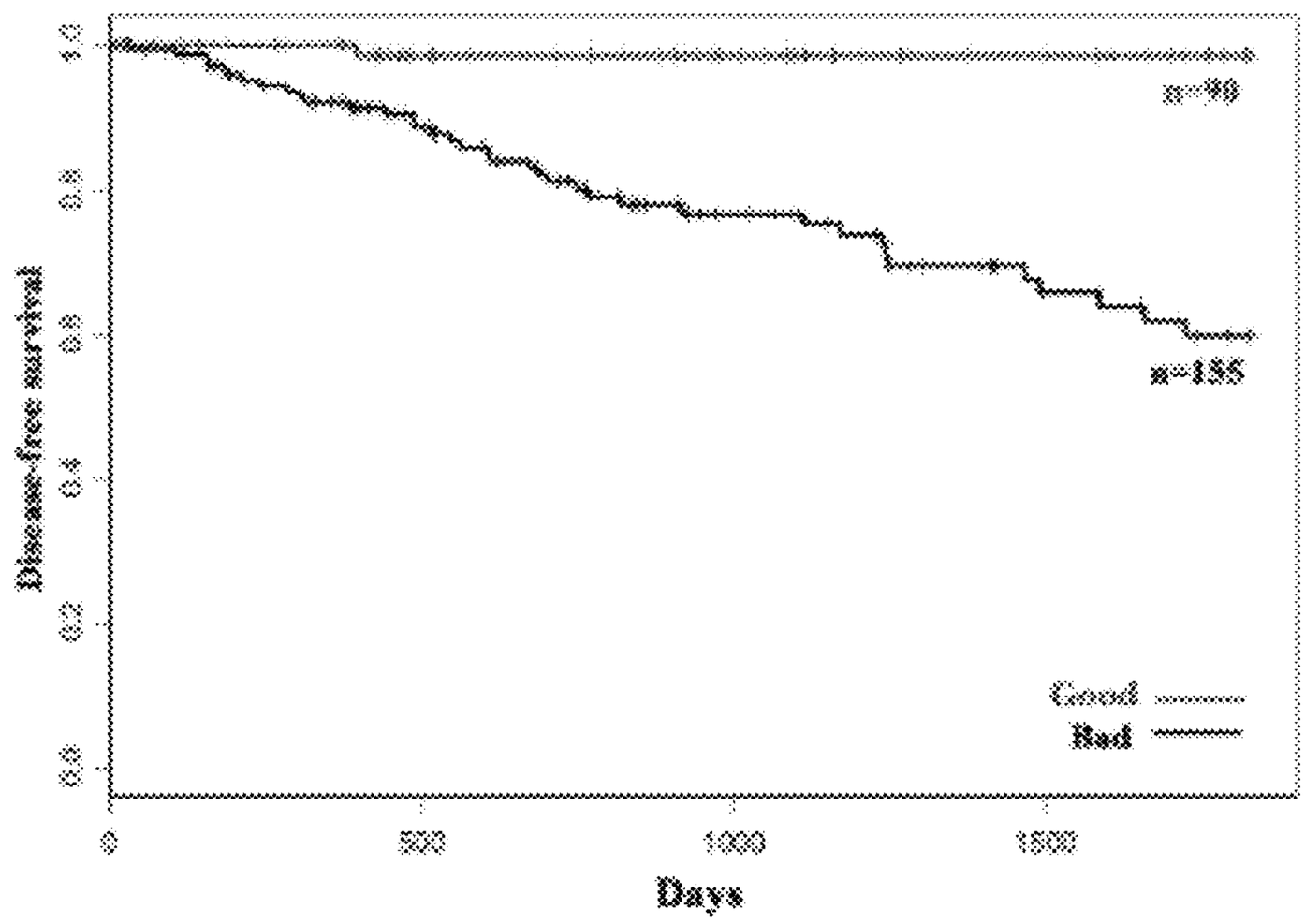


FIGURE 13

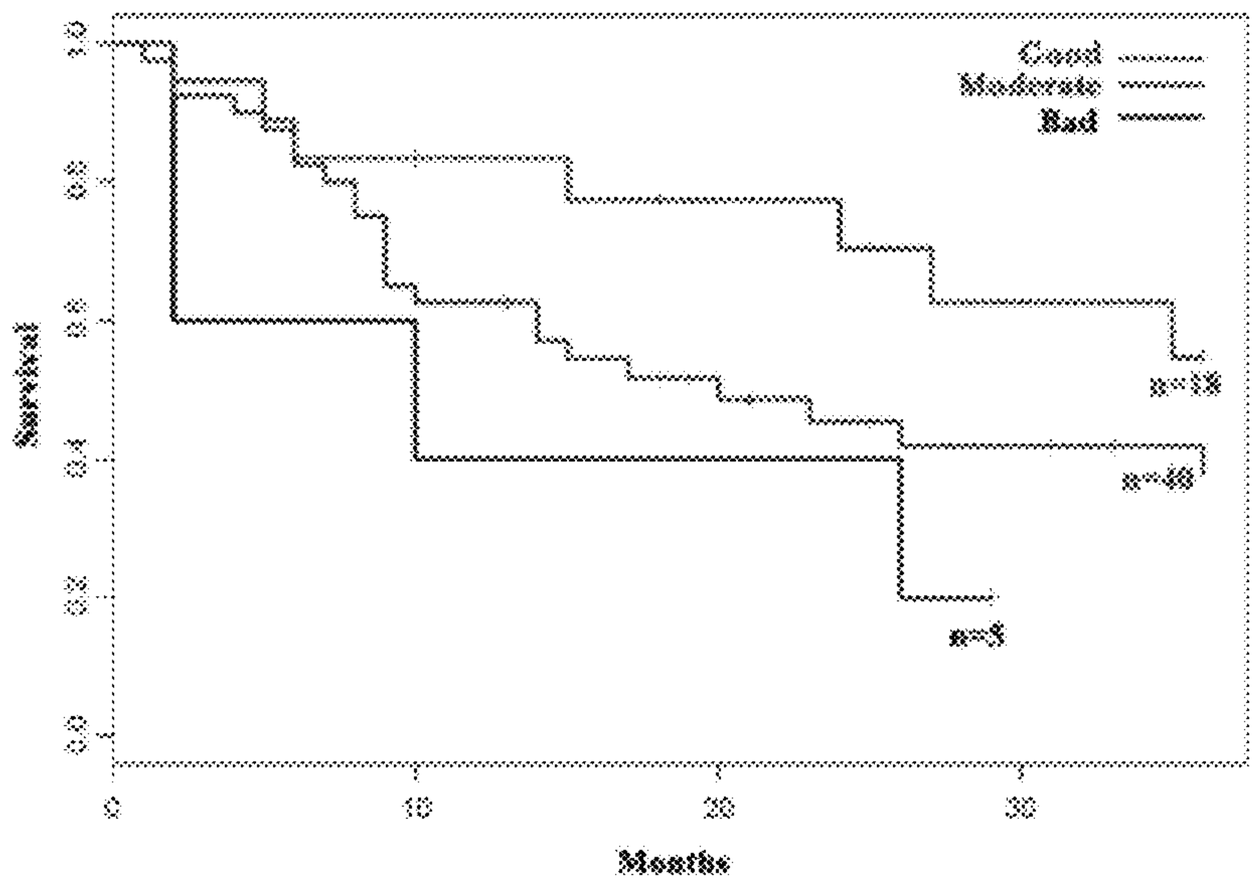


FIGURE 14

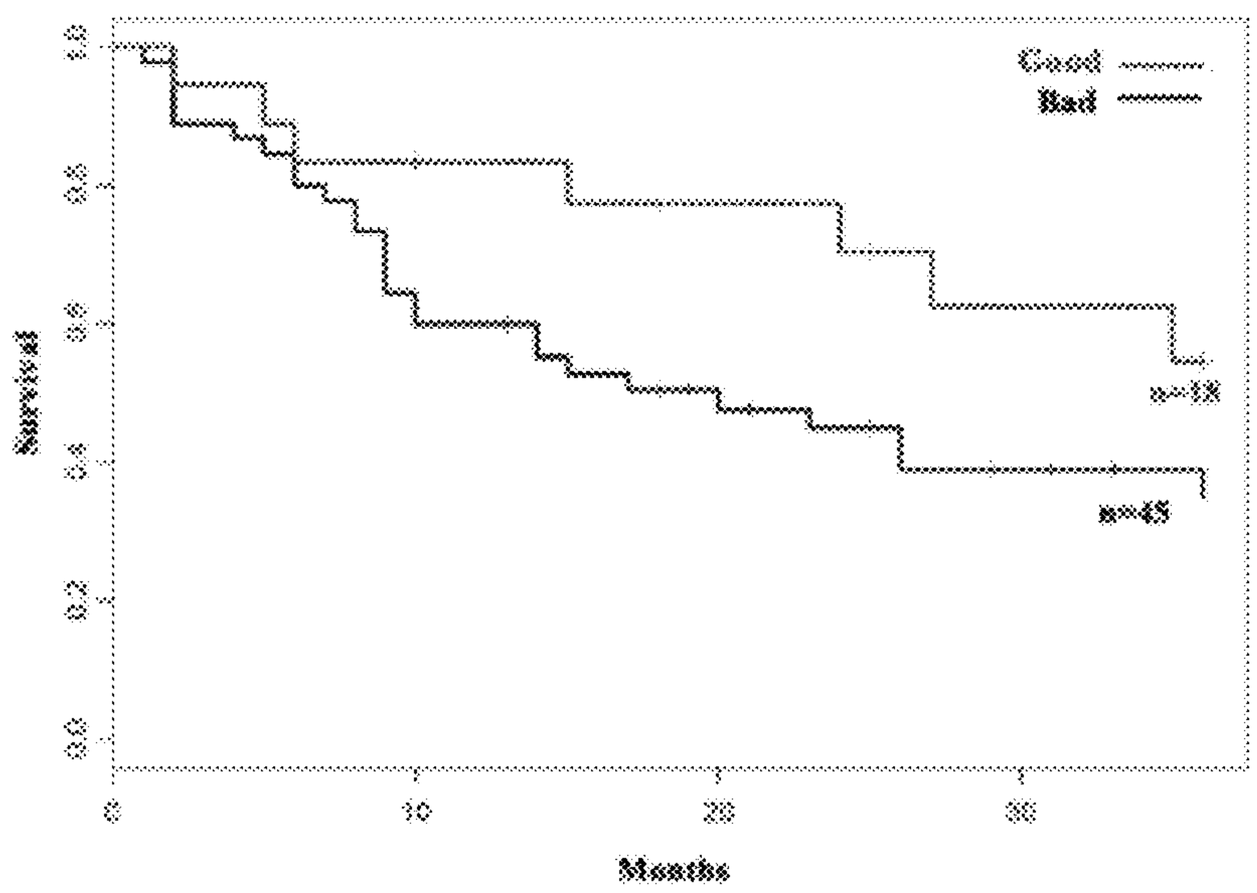


FIGURE 15

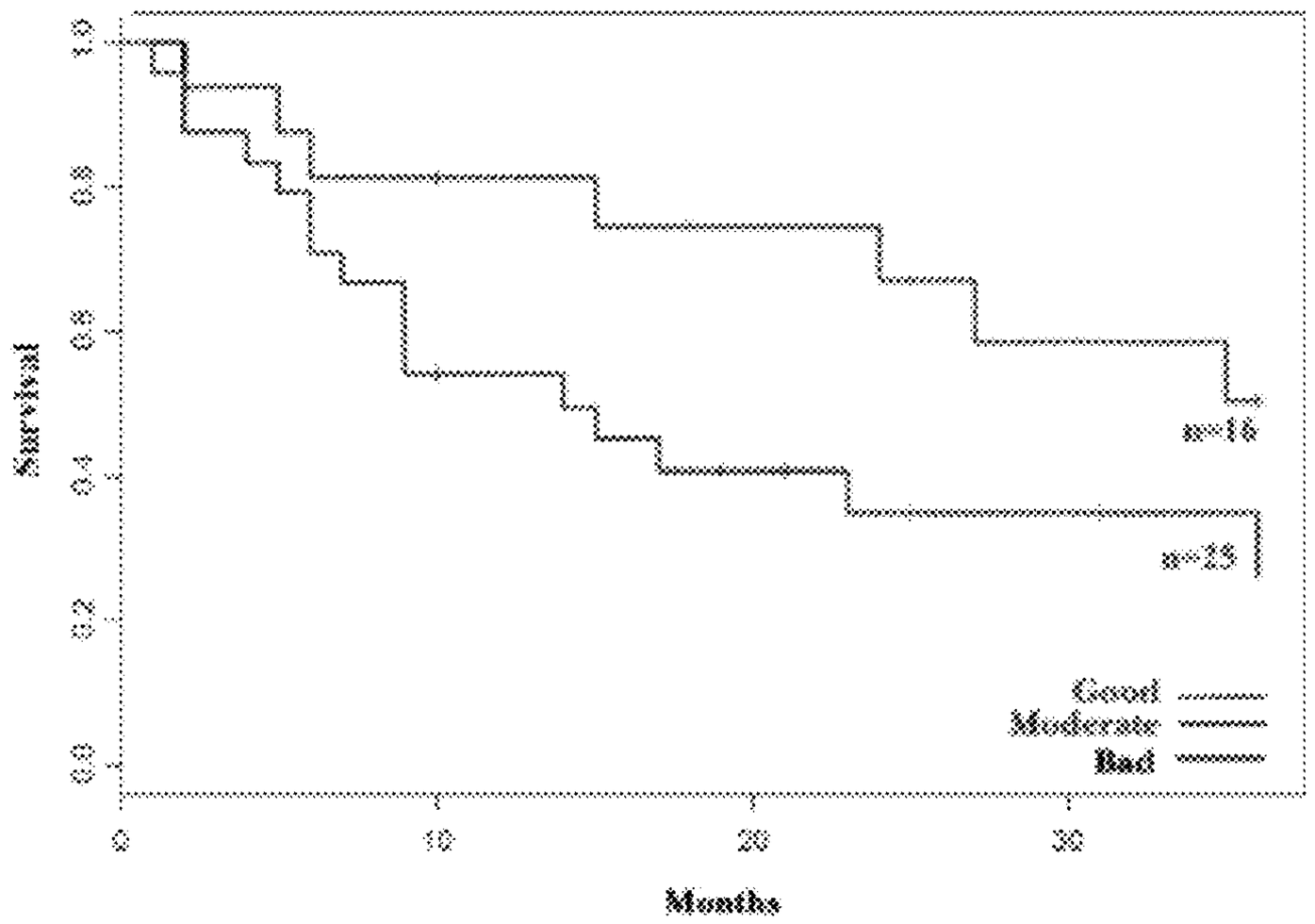


FIGURE 16

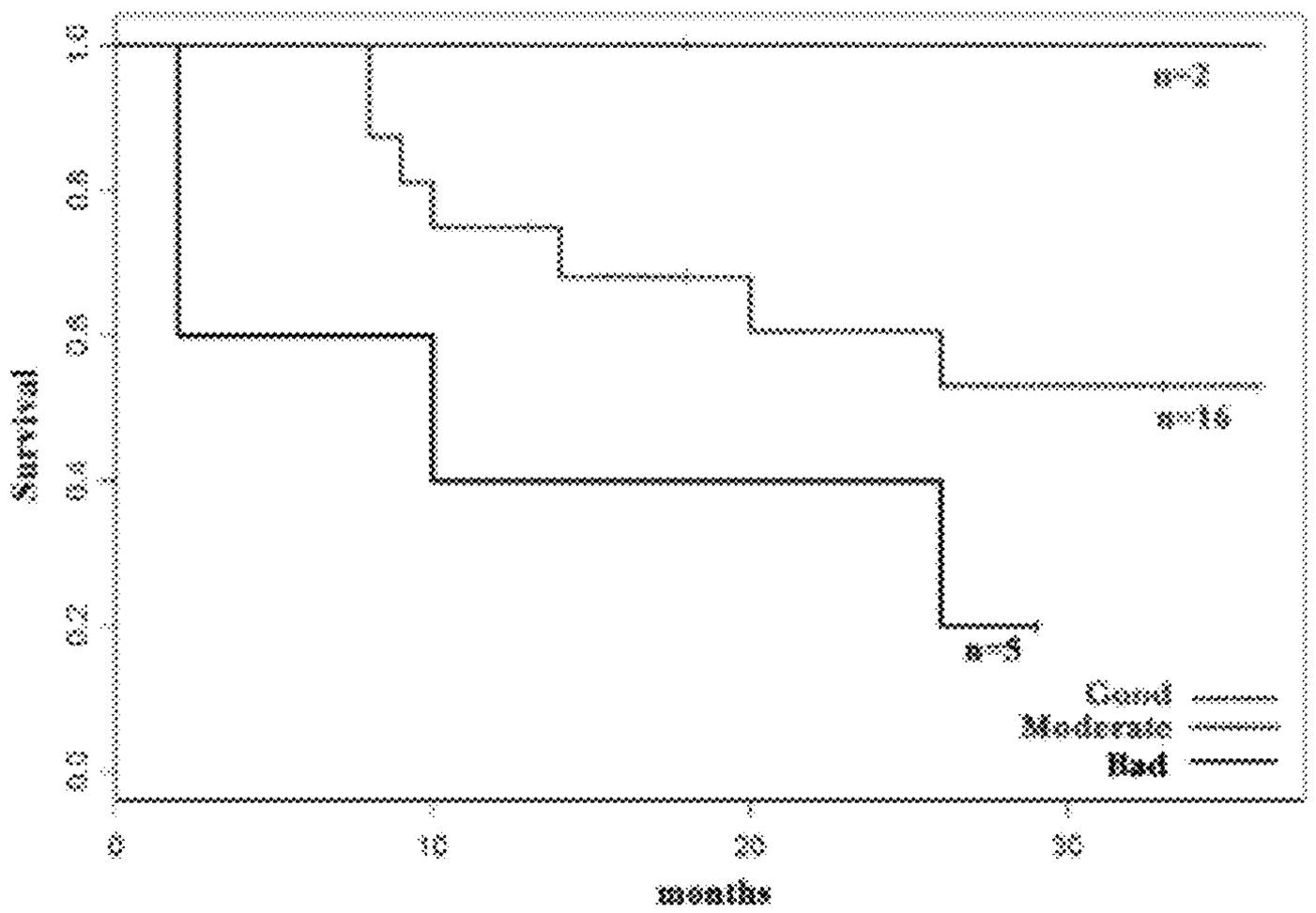


FIGURE 17

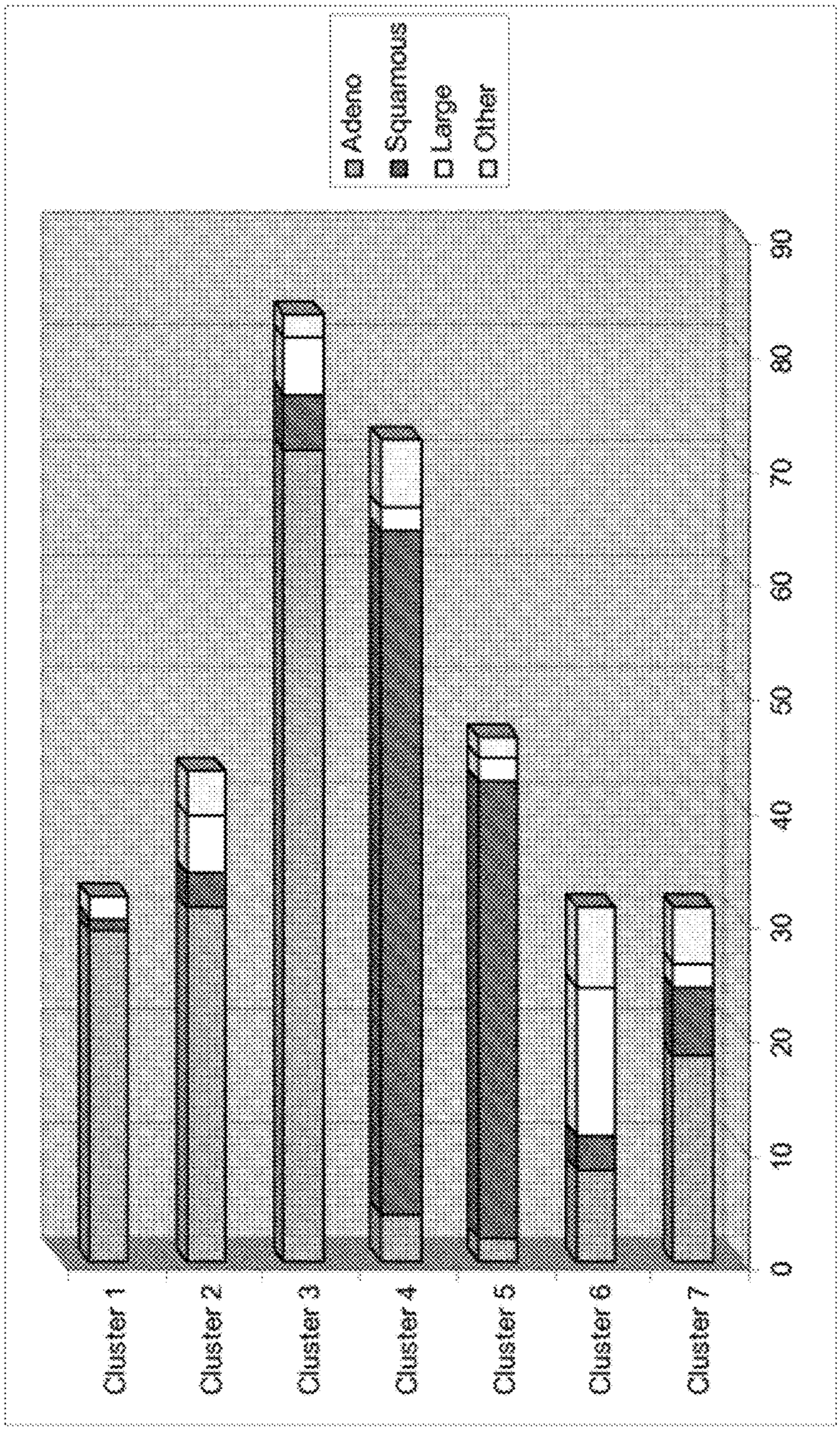

Adeno
Squamous
Large
Other
Cluster 1
Cluster 2
Cluster 3
Cluster 4
Cluster 5
Cluster 6
Cluster 7
0
10
20
30
40
50
60
70
80
90

FIGURE 18

REAGENTS AND METHODS FOR USE IN CANCER DIAGNOSIS, CLASSIFICATION AND THERAPY

PRIORITY INFORMATION

This application is a divisional application of U.S. Ser. No. 12/879,356 filed Sep. 10, 2010, which is a divisional application of U.S. Ser. No. 12/013,739 filed Jan. 14, 2008, (now U.S. Pat. No. 7,811,774),which is a divisional application of U.S. Ser. No. 11/061,067 filed Feb. 18, 2005 now abandoned, which is a continuation-in-part of U.S. Ser. No. 10/915,059 filed Aug. 10, 2004 now abandoned which claimed priority to U.S. Ser. No. 60/494,334 filed Aug. 11, 2003 and U.S. Ser. No. 60/570,206 filed May 12, 2004. The entire contents of each of these applications are hereby incorporated by reference.

SEQUENCE LISTING

In accordance with 37 CFR 1.52(e)(5), a Sequence Listing in the form of a text file (entitled "Sequence Listing.txt," created on Sep. 7, 2010, and 93 kilobytes) is incorporated herein by reference in its entirety.

BACKGROUND OF THE INVENTION

A major challenge of cancer treatment is the selection of therapeutic regimens that maximize efficacy and minimize toxicity for a given patient. A related challenge lies in the attempt to provide accurate diagnostic, prognostic and predictive information. At present, tumors are generally classified under the tumor-node-metastasis (TNM) system. This system, which uses the size of the tumor, the presence or absence of tumor in regional lymph nodes, and the presence or absence of distant metastases, to assign a stage to the tumor is described in the *AJCC Cancer Staging Manual*, Lippincott, 5th ed., pp. 171-180 (1997). The assigned stage is used as a basis for selection of appropriate therapy and for prognostic purposes. In addition to the TNM parameters, morphologic appearance is used to further classify tumors into tumor types and thereby aid in selection of appropriate therapy. However, this approach has serious limitations. Tumors with similar histopathologic appearance can exhibit significant variability in terms of clinical course and response to therapy. For example, some tumors are rapidly progressive while others are not. Some tumors respond readily to hormonal therapy or chemotherapy while others are resistant.

Assays for cell surface markers, e.g., using immunohistochemistry, have provided means for dividing certain tumor types into subclasses. For example, one factor considered in prognosis and treatment decisions for breast cancer is the presence or absence of the estrogen receptor (ER) in tumor samples. ER-positive breast cancers typically respond much more readily to hormonal therapies such as tamoxifen, which acts as an anti-estrogen in breast tissue, than ER-negative tumors. Though useful, these analyses only in part predict the clinical behavior of breast tumors. There is phenotypic diversity present in cancers that current diagnostic tools fail to detect. As a consequence, there is still much controversy over how to stratify patients amongst potential treatments in order to optimize outcome (e.g., for breast cancer see "NIH Consensus Development Conference Statement: Adjuvant Therapy for Breast Cancer, Nov. 1-3, 2000", *J. Nat. Cancer Inst. Monographs,* 30:5-15, 2001 and Di Leo et al., *Int. J. Clin. Oncol.* 7:245-253, 2002).

There clearly exists a need for improved methods and reagents for classifying tumors. Once these methods and reagents are available, clinical studies can be performed that will allow the identification of classes or subclasses of patients having different prognosis and/or responses to therapy. Such prognostic tools will allow more rationally based choices governing the aggressiveness of therapeutic interventions; such predictive tools will also be useful for directing patients into appropriate treatment protocols.

SUMMARY OF THE INVENTION

The invention encompasses the realization that particular panels of tumor sample binding agents ("interaction partners") can be used to provide new insights into the biology of cancer. Among other things, the present invention provides methods and reagents for classifying tumors and for identifying new tumor classes and subclasses. The invention further provides methods for correlating tumor class or subclass with therapeutic regimen or outcome, for identifying appropriate (new or known) therapies for particular classes or subclasses, and for predicting outcomes based on class or subclass. The invention further provides new therapeutic agents and methods for the treatment of cancer.

For example, the present invention provides methods for identifying suitable panels of interaction partners (e.g., without limitation antibodies) whose binding is correlated with any of a variety of desirable aspects such as tumor class or subclass, tumor source (e.g., primary tumor versus metastases), likely prognosis, responsiveness to therapy, etc. Specifically, collections of interaction partners are selected and their activity in binding to a variety of different tumors, normal tissues and/or cell lines is assessed. Data are collected for multiple interaction partners to multiple samples and correlations with interesting or desirable features are assessed. As described herein, the detection of individual interaction partners or panels thereof that bind differentially with different tumors provides new methods of use in cancer prognosis and treatment selection. In addition, these interaction partners provide new therapies for treating cancer.

As described in further detail below, the invention employs methods for grouping interaction partners within a panel into subsets by determining their binding patterns across a collection of samples obtained from different tumor tissues, normal tissues and/or cell lines. The invention also groups the tumor samples into classes or subclasses based on similarities in their binding to a panel of interaction partners. This two-dimensional grouping approach permits the association of particular classes of tumors with particular subsets of interaction partners that, for example, show relatively high binding to tumors within that class. Correlation with clinical information indicates that the tumor classes have clinical significance in terms of prognosis or response to chemotherapy.

BRIEF DESCRIPTION OF APPENDICES A-F

This patent application refers to material comprising tables and data presented as appendices.

Appendix A is a table that lists the antibodies included in the breast, lung and/or colon panels that are discussed in the Examples. The table includes the antibody ID, parent gene name, NCBI LocusLink ID, UniGene ID, known aliases for the parent gene, peptides that were used in preparing antibodies, antibody titer and a link to any relevant IHC images of Appendix B. Using the parent gene name, NCBI LocusLink ID, UniGene ID, and/or known aliases for the parent gene, a

skilled person can readily obtain the nucleotide (and corresponding amino acid) sequences for each and every one of the parent genes that are listed in Appendix A from a public database (e.g., GenBank, Swiss-Prot or any future derivative of these). The nucleotide and corresponding amino acid sequences for each and every one of the parent genes that are listed in Appendix A are hereby incorporated by reference from these public databases. Antibodies with AGI IDs that begin with s5 or s6 were obtained from commercial sources as indicated. The third and fourth columns of Appendix A indicate whether the antibodies of the breast cancer classification panel were identified by staining with the Russian breast cohort (Example 2) and/or the HH breast cohort (Example 3). The fifth and sixth columns indicate whether the antibodies of the lung cancer classification panel were identified by staining with the Russian lung cohort (Example 4) and/or the HH lung cohort (Example 5). The seventh column indicates the antibodies of the colon cancer classification panel. These were all identified by staining with the Russian colon cohort (Example 6).

Appendix B includes breast IHC images, colon IHC images and lung IHC images. The IHC images of Appendix B are referenced in the right hand column of Appendix A. An actual copy of Appendix B is not included with this continuation-in-part but can be found in parent case U.S. Ser. No. 10/915,059 filed Aug. 10, 2004 (published as US 2005/0112662 on May 26, 2005), the entire contents of which are hereby incorporated by reference.

Appendix C is a table that lists exemplary antibodies whose binding patterns have been shown to correlate with tumor prognosis in breast cancer patients. The results are grouped into four categories that have been clinically recognized to be of significance: all patients, ER+ patients, ER− patients, and ER+/lymph node metastases negative (ER+/node−) patients. Scoring methods 1-3 use the following schemes: method 1 (0=negative; 1=weak; 2=strong); method 2 (0=negative; 1=weak or strong); and method 3 (0=negative or weak; 1=strong). This table was prepared using samples from the HH breast cohort as described in Example 10.

Appendix D is a table that lists exemplary antibodies whose binding patterns have been shown to correlate with tumor prognosis in lung cancer patients. The results are grouped into three categories that have been clinically recognized to be of significance: all patients, adenocarcinoma patients, and squamous cell carcinoma patients. Scoring methods 1-3 use the following schemes: method 1 (0=negative; 1=weak; 2=strong); method 2 (0=negative; 1=weak or strong); and method 3 (0=negative or weak; 1=strong).

Appendix E is a table that lists exemplary antibodies whose binding patterns have been shown to correlate with tumor prognosis in breast cancer patients. The results are grouped into four categories that have been clinically recognized to be of significance: all patients, ER+ patients, ER− patients, and ER+/lymph node metastases negative (ER+/node−) patients. Scoring methods 1-3 use the following schemes: method 1 (0=negative; 1=weak; 2=strong); method 2 (0=negative; 1=weak or strong); and method 3 (0=negative or weak; 1=strong). This table was prepared using samples from the HH breast cohort as described in Example 12. Appendix E differs from Appendix C because of further analysis.

Appendix F is a table that lists exemplary antibodies whose binding patterns have been shown to correlate with tumor prognosis in lung cancer patients. The results are grouped into two categories that have been clinically recognized to be of significance: all patients and adenocarcinoma patients. Scoring methods 1-3 use the following schemes: method 1 (0=negative; 1=weak; 2=strong); method 2 (0=negative; 1=weak or strong); and method 3 (0=negative or weak; 1=strong). This table was prepared using samples from the HH and UAB lung cohorts as described in Example 13. The p-values and hazard ratios that were obtained with each cohort are shown. The antibodies listed have a prognostic p-value of less than 0.2 in both cohorts.

BRIEF DESCRIPTION OF THE DRAWING

FIG. **1** depicts semi-quantitative immunohistochemistry (IHC) scoring of a 298 breast cancer patient cohort with an inventive breast cancer classification panel. The panel was prepared as described in Example 2—antibodies were used as interaction partners. The patients (rows) were classified using k-means clustering while the antibodies (columns) were organized using hierarchical clustering. Dark gray represents strong positive staining, black represents weak positive staining, while light gray represents the absence of staining and medium gray represents a lack of data. As illustrated in the Figure, nine groups of patients were identified by their consensus pattern of staining with the panel of antibodies.

FIG. **2** depicts semi-quantitative immunohistochemistry (IHC) scoring of a 387 lung cancer patient cohort with an inventive lung cancer classification panel. The panel was prepared as described in Example 4—antibodies were used as interaction partners. The patients (rows) were classified using k-means clustering while the antibodies (columns) were organized using hierarchical clustering. Dark gray represents strong positive staining, black represents weak positive staining, while light gray represents the absence of staining and medium gray represents a lack of data. As illustrated in the Figure, eight groups of patients were identified by their consensus pattern of staining with the panel of antibodies.

FIG. **3** depicts semi-quantitative immunohistochemistry (IHC) scoring of a 359 colon cancer patient cohort with an inventive colon cancer classification panel. The panel was prepared as described in Example 6—antibodies were used as interaction partners. The patients (rows) were classified using k-means clustering while the antibodies (columns) were organized using hierarchical clustering. Dark gray represents strong positive staining, black represents weak positive staining, while light gray represents the absence of staining and medium gray represents a lack of data. As illustrated in the Figure, seven groups of patients were identified by their consensus pattern of staining with the panel of antibodies.

FIG. **4** shows Kaplan-Meier curves that were generated for ER+ patients after prognostic classification based on (A) staining with a prognostic panel of antibodies from Appendix C and (B) the Nottingham Prognostic Index (NPI). In each case the patients were placed into one of three prognostic groups, namely "poor" (bottom curve), "moderate" (middle curve) and "good" (top curve).

FIG. **5** shows Kaplan-Meier curves that were generated for ER+/node− patients after prognostic classification based on (A) staining with a prognostic panel of antibodies from Appendix C and (B) the Nottingham Prognostic Index (NPI). In each case the patients were placed into one of three prognostic groups, namely "poor" (bottom curve), "moderate" (middle curve) and "good" (top curve). Note that under the NPI scheme ER+/node− patients are never categorized as having a "poor" prognosis. For this reason, FIG. **5**B only includes curves for patients with a "moderate" or "good" prognosis.

FIG. **6** shows Kaplan-Meier curves that were generated for ER+/node− patients after prognostic classification based on staining with the exemplary prognostic panel of antibodies from Table 5. In each case the patients were placed into one of

three prognostic groups, namely "bad" (bottom curve), "moderate" (middle curve) and "good" (top curve).

FIG. **7** shows Kaplan-Meier curves that were generated for ER− patients after prognostic classification based on staining with the exemplary prognostic panel of antibodies from Table 6. In each case the patients were placed into one of three prognostic groups, namely "bad" (bottom curve), "moderate" (middle curve) and "good" (top curve).

FIG. **8** shows Kaplan-Meier curves that were generated for ER− patients after prognostic classification based on staining with the exemplary prognostic panel of antibodies from Table 7. In each case the patients were placed into one of three prognostic groups, namely "bad" (bottom curve), "moderate" (middle curve) and "good" (top curve).

FIG. **9** shows a dendrogram for the tree panel of Table 8 that may be used for the prognostic classification of ER+/node− patients. If a patient is positive for staining at a given node his or her prognosis decision tree follows the branch marked with a "+". Conversely if a patient is negative for staining at a given node his or her prognosis decision tree follows the branch marked "−". This is done until a terminus is reached.

FIG. **10** shows Kaplan-Meier curves that were generated for ER+/node− patients after prognostic classification based on staining with the exemplary prognostic panel of antibodies from Table 8. In each case the patients were placed into one of three prognostic groups, namely "bad" (bottom curve), "moderate" (middle curve) and "good" (top curve).

FIG. **11** shows a dendrogram for the tree panels of Table 9 that may be used for the prognostic classification of ER+ and ER− patients. If a patient is positive for staining at a given node his or her prognosis decision tree follows the branch marked with a "+". Conversely if a patient is negative for staining at a given node his or her prognosis decision tree follows the branch marked "−". This is done until a terminus is reached.

FIG. **12** shows Kaplan-Meier curves that were generated for combined lung cancer patients (HH cohort) after prognostic classification with the exemplary prognostic panels of antibodies from Tables 10 and 11. In each case the patients were placed into one of three prognostic groups, namely "bad" (bottom curve), "moderate" (middle curve) and "good" (top curve).

FIG. **13** shows the curves that were obtained when patients in the "moderate" and "bad" groups of FIG. **12** were combined into a single "bad" prognostic group.

FIG. **14** shows Kaplan-Meier curves that were generated for combined lung cancer patients (UAB cohort) after prognostic classification with the exemplary prognostic panels of antibodies from Tables 10 and 11. In each case the patients were placed into one of three prognostic groups, namely "bad" (bottom curve), "moderate" (middle curve) and "good" (top curve).

FIG. **15** shows the curves that were obtained when the patients in the "moderate" and "bad" groups of FIG. **14** were combined into a single "bad" prognostic group.

FIG. **16** shows Kaplan-Meier curves that were generated for adenocarcinoma patients (UAB cohort) after prognostic classification with the exemplary prognostic panels of antibodies from Table 11. In each case the patients were placed into one of three prognostic groups, namely "bad" (bottom curve), "moderate" (middle curve) and "good" (top curve).

FIG. **17** shows Kaplan-Meier curves that were generated for squamous cell carcinoma patients (UAB cohort) after prognostic classification with the exemplary prognostic panels of antibodies from Table 10. In each case the patients were placed into one of three prognostic groups, namely "bad" (bottom curve), "moderate" (middle curve) and "good" (top curve).

FIG. **18** shows the relative proportions of different lung cancer morphologies that were identified in seven sub-classes of patients in the HH lung cohort.

DEFINITIONS

Associated—When an interaction partner and a tumor marker are physically "associated" with one another as described herein, they are linked by direct non-covalent interactions. Desirable non-covalent interactions include those of the type which occur between an immunoglobulin molecule and an antigen for which the immunoglobulin is specific, for example, ionic interactions, hydrogen bonds, van der Waals interactions, hydrophobic interactions, etc. The strength, or affinity of the physical association can be expressed in terms of the dissociation constant (K_d) of the interaction, wherein a smaller K_d represents a greater affinity. The association properties of selected interaction partners and tumor markers can be quantified using methods well known in the art (e.g., see Davies et al., *Annual Rev. Biochem.* 59:439, 1990).

Classification panel—A "classification panel" of interaction partners is a set of interaction partners whose collective pattern of binding or lack of binding to a tumor sample, when taken together, is sufficient to classify the tumor sample as a member of a particular class or subclass of tumor, or as not a member of a particular class or subclass of tumor.

Correlation—"Correlation" refers to the degree to which one variable can be predicted from another variable, e.g., the degree to which a patient's therapeutic response can be predicted from the pattern of binding between a set of interaction partners and a tumor sample taken from that patient. A variety of statistical methods may be used to measure correlation between two variables, e.g., without limitation the student t-test, the Fisher exact test, the Pearson correlation coefficient, the Spearman correlation coefficient, the Chi squared test, etc. Results are traditionally given as a measured correlation coefficient with a p-value that provides a measure of the likelihood that the correlation arose by chance. A correlation with a p-value that is less than 0.05 is generally considered to be statistically significant. Preferred correlations have p-values that are less than 0.01, especially less than 0.001.

Interaction partner—An "interaction partner" is an entity that physically associates with a tumor marker. For example and without limitation, an interaction partner may be an antibody or a fragment thereof that physically associates with a tumor marker. In general, an interaction partner is said to "associate specifically" with a tumor marker if it associates at a detectable level with the tumor marker and does not associate detectably with unrelated molecular entities (e.g., other tumor markers) under similar conditions. Specific association between a tumor marker and an interaction partner will typically be dependent upon the presence of a particular structural feature of the target tumor marker such as an antigenic determinant or epitope recognized by the interaction partner. Generally, if an interaction partner is specific for epitope A, the presence of a molecular entity (e.g., a protein) containing epitope A or the presence of free unlabeled A in a reaction containing both free labeled A and the interaction partner thereto, will reduce the amount of labeled A that binds to the interaction partner. In general, it is to be understood that specificity need not be absolute. For example, it is well known in the art that antibodies frequently cross-react with other epitopes in addition to the target epitope. Such cross-reactivity may be acceptable depending upon the application for

which the interaction partner is to be used. Thus the degree of specificity of an interaction partner will depend on the context in which it is being used. In general, an interaction partner exhibits specificity for a particular tumor marker if it favors binding with that partner above binding with other potential partners, e.g., other tumor markers. One of ordinary skill in the art will be able to select interaction partners having a sufficient degree of specificity to perform appropriately in any given application (e.g., for detection of a target tumor marker, for therapeutic purposes, etc.). It is also to be understood that specificity may be evaluated in the context of additional factors such as the affinity of the interaction partner for the target tumor marker versus the affinity of the interaction partner for other potential partners, e.g., other tumor markers. If an interaction partner exhibits a high affinity for a target tumor marker and low affinity for non-target molecules, the interaction partner will likely be an acceptable reagent for diagnostic purposes even if it lacks specificity. It will be appreciated that once the specificity of an interaction partner is established in one or more contexts, it may be employed in other, preferably similar, contexts without necessarily re-evaluating its specificity.

Predictive panel—A "predictive panel" of interaction partners is a set of interaction partners whose collective pattern of binding or lack of binding to a tumor sample, when taken together, has sufficient correlation to classify the tumor sample as being from a patient who is likely (or not) to respond to a given therapeutic regimen.

Prognostic panel—A "prognostic panel" of interaction partners is a set of interaction partners whose collective pattern of binding or lack of binding to a tumor sample, when taken together, has sufficient correlation to classify the tumor sample as being from a patient who is likely to have a given outcome. Generally, "outcome" may include, but is not limited to, the average life expectancy of the patient, the likelihood that the patient will survive for a given amount of time (e.g., 6 months, 1 year, 5 years, etc.), the likelihood of recurrence, the likelihood that the patient will be disease-free for a specified prolonged period of time, or the likelihood that the patient will be cured of the disease.

Response—The "response" of a tumor or a cancer to therapy may represent any detectable change, for example at the molecular, cellular, organellar, or organismal level. For instance, tumor size, patient life expectancy, recurrence, or the length of time the patient survives, etc., are all responses. Responses can be measured in any of a variety of ways, including for example non-invasive measuring of tumor size (e.g., CT scan, image-enhanced visualization, etc.), invasive measuring of tumor size (e.g., residual tumor resection, etc.), surrogate marker measurement (e.g., serum PSA, etc.), clinical course variance (e.g., measurement of patient quality of life, time to relapse, survival time, etc.).

Small molecule—A "small molecule" is a non-polymeric molecule. A small molecule can be synthesized in a laboratory (e.g., by combinatorial synthesis) or found in nature (e.g., a natural product). A small molecule is typically characterized in that it contains several carbon-carbon bonds and has a molecular weight of less than about 1500 Da, although this characterization is not intended to be limiting for the purposes of the present invention.

Tumor markers—"Tumor markers" are molecular entities that are detectable in tumor samples. Generally, tumor markers will be proteins that are present within the tumor sample, e.g., within the cytoplasm or membranes of tumor cells and/or secreted from such cells. According to the present invention, sets of tumor markers that correlate with tumor class or subclass are identified. Thus, subsequent tumor samples may be classified or subclassified based on the presence of these sets of tumor markers.

Tumor sample—As used herein the term "tumor sample" is taken broadly to include cell or tissue samples removed from a tumor, cells (or their progeny) derived from a tumor that may be located elsewhere in the body (e.g., cells in the bloodstream or at a site of metastasis), or any material derived by processing such a sample. Derived tumor samples may include, for example, nucleic acids or proteins extracted from the sample.

DETAILED DESCRIPTION OF CERTAIN PREFERRED EMBODIMENTS OF THE INVENTION

As noted above, the present invention provides techniques and reagents for the classification and subclassification, of tumors. Such classification (or subclassification) has many beneficial applications. For example, a particular tumor class or subclass may correlate with prognosis and/or susceptibility to a particular therapeutic regimen. As such, the classification or subclassification may be used as the basis for a prognostic or predictive kit and may also be used as the basis for identifying previously unappreciated therapies. Therapies that are effective against only a particular class or subclass of tumor may have been lost in studies whose data were not stratified by subclass; the present invention allows such data to be re-stratified, and allows additional studies to be performed, so that class- or subclass-specific therapies may be identified and/or implemented. Alternatively or additionally, the present invention allows identification and/or implementation of therapies that are targeted to genes identified as class- or subclass-specific.

Classification and Subclassification of Tumors

In general, according to the present invention, tumors are classified or subclassified on the basis of tumor markers whose presence is correlated with a particular class or subclass. In preferred embodiments, the tumor markers are detected via their physical association with an interaction partner. Included in the present invention are kits comprising sets of interaction partners that together can be used to identify or classify a particular tumor sample; such sets are generally referred to as "classification panels".

The present invention provides systems of identifying classification panels. In general, tumor samples are contacted with individual interaction partners, and binding between the interaction partners and their cognate tumor markers is detected. For example, panels of interaction partners that identify a particular class or subclass of tumor within tumor samples of a selected tissue of origin may be defined by contacting individual interaction partners with a variety of different tumor samples (e.g., from different patients) all of the same tissue of origin. Individual interaction partners may be selected for inclusion in the ultimate classification panel based on their binding to only a subset of the tumor samples (e.g., see Examples 1-4). Those of ordinary skill in the art, however, will appreciate that all that is required for a collection of interaction partners to operate effectively as a classification panel is that the combined binding characteristics of member interaction partners together are sufficient to classify a particular tumor sample.

The inventive process of identifying useful panels of interaction partners as described herein may itself result in the identification of new tumor classes or subclasses. That is, through the process of analyzing interaction partner binding patterns, investigators will often discover new tumor classes

or subclasses to which sets of interaction partners bind. Thus, the processes (a) of defining classification panels of interaction partners for given tumor classes or subclasses; and (b) identifying new tumor classes or subclasses may well be experimentally interrelated. In general, the greater the number of tumor samples tested, the greater the likelihood that new classes or subclasses will be defined.

Often, when identifying sets of interaction partners that can act as a classification (or subclassification) panel, it will be desirable to obtain the largest set of tumor samples possible, and also to collect the largest amount of information possible about the individual samples. For example, the origin of the tumor, the gender of the patient, the age of the patient, the staging of the tumor (e.g., according to the TNM system), any microscopic or submicroscopic characteristics of the tumor that may have been determined, may be recorded. Those of ordinary skill in the art will appreciate that the more information that is known about a tumor sample, the more aspects of that sample are available for correlation with interaction partner binding.

The systems of the present invention have particular utility in classifying or subclassifying tumor samples that are not otherwise distinguishable from one another. Thus, in some embodiments, it will be desirable to analyze the largest collection of tumor samples that are most similar to one another.

When obtaining tumor samples for testing according to the present invention, it is generally preferred that the samples represent or reflect characteristics of a population of patients or samples. It may also be useful to handle and process the samples under conditions and according to techniques common to clinical laboratories. Although the present invention is not intended to be limited to the strategies used for processing tumor samples, we note that, in the field of pathology, it is often common to fix samples in buffered formalin, and then to dehydrate them by immersion in increasing concentrations of ethanol followed by xylene. Samples are then embedded into paraffin, which is then molded into a "paraffin block" that is a standard intermediate in histologic processing of tissue samples. The present inventors have found that many useful interaction partners display comparable binding regardless of the method of preparation of tumor samples; those of ordinary skill in the art can readily adjust observations to account for differences in preparation procedure.

In preferred embodiments of the invention, large numbers of tissue samples are analyzed simultaneously. In some embodiments, a tissue array is prepared. Tissue arrays may be constructed according to a variety of techniques. According to one procedure, a commercially-available mechanical device (e.g., the manual tissue arrayer MTA1 from Beecher Instruments of Sun Prairie, Wis.) is used to remove an 0.6-micron-diameter, full thickness "core" from a paraffin block (the donor block) prepared from each patient, and to insert the core into a separate paraffin block (the recipient block) in a designated location on a grid. In preferred embodiments, cores from as many as about 400 patients can be inserted into a single recipient block; preferably, core-to-core spacing is approximately 1 mm. The resulting tissue array may be processed into thin sections for staining with interaction partners according to standard methods applicable to paraffin embedded material. Depending upon the thickness of the donor blocks, as well as the dimensions of the clinical material, a single tissue array can yield about 50-150 slides containing >75% relevant tumor material for assessment with interaction partners. Construction of two or more parallel tissue arrays of cores from the same cohort of patient samples can provide relevant tumor material from the same set of patients in duplicate or more. Of course, in some cases, additional samples will be present in one array and not another.

The present inventors have found that it is often desirable to evaluate some aspects of the binding characteristics of potential interaction partners before or while assessing the desirability of including them in an interaction panel. For example, the inventors have found that it is often desirable to perform a titration study in which different concentrations of the interaction partner are contacted with a diverse set of tissue samples derived from a variety of different tissues (e.g., normal and/or tumor) in order to identify a concentration or titer at which differential binding is observed. This titer is referred to herein as a "discriminating titer". Such differential staining may be observed between different tissue samples and/or between different cell types within a given tissue sample.

In general, any tissue sample may be used for this purpose (e.g., samples obtained from the epididymis, esophagus, gall bladder, kidneys, liver, lungs, lymph nodes, muscles, ovaries, pancreas, parathyroid glands, placenta, prostate, saliva, skin, spleen, stomach, testis, thymus, thyroid, tonsils, uterus, etc.). For such titration studies, greater diversity among samples is often preferred. Without intending to limit the present invention, the inventors observe that useful titers for particular interaction partners can typically be defined in a study of approximately 40-70 different tissue samples from about 20-40 different tissues.

Binding studies (for titration, for assessment of inclusion in a panel, or during use of a panel) may be performed in any format that allows specific interaction to be detected. Where large numbers of samples are to be handled, it may be desirable to utilize arrayed and/or automated formats. Particularly preferred formats include tissue arrays as discussed above. The staining of large numbers of samples derived from a variety of tumors in a tissue array format allows excellent comparative assessment of differential staining between or among samples under identical conditions. According to the present invention, staining patterns that identify at least about 10% of samples as binding with a particular interaction partner, or at least about 20, 30, 40, 50% or more of samples, are likely to represent "real" differential staining patterns (i.e., real variations in binding with interaction partner and not experimental variations, for example, due to sample processing or day to day variation in staining techniques).

Any available technique may be used to detect binding between an interaction partner and a tumor sample. One powerful and commonly used technique is to have a detectable label associated (directly or indirectly) with the interaction partner. For example, commonly-used labels that often are associated with antibodies used in binding studies include fluorochromes, enzymes, gold, iodine, etc. Tissue staining by bound interaction partners is then assessed, preferably by a trained pathologist or cytotechnologist. For example, a scoring system may be utilized to designate whether the interaction partner does or does not bind to (e.g., stain) the sample, whether it stains the sample strongly or weakly and/or whether useful information could not be obtained (e.g., because the sample was lost, there was no tumor in the sample or the result was otherwise ambiguous). Those of ordinary skill in the art will recognize that the precise characteristics of the scoring system are not critical to the invention. For example, staining may be assessed qualitatively or quantitatively; more or less subtle gradations of staining may be defined; etc.

Whatever the format, and whatever the detection strategy, identification of a discriminating titer can simplify binding studies to assess the desirability of including a given interaction partner in a panel. In such studies, the interaction partner

is contacted with a plurality of different tumor samples that preferably have at least one common trait (e.g., tissue of origin), and often have multiple common traits (e.g., tissue of origin, stage, microscopic characteristics, etc.). In some cases, it will be desirable to select a group of samples with at least one common trait and at least one different trait, so that a panel of interaction partners is defined that distinguishes the different trait. In other cases, it will be desirable to select a group of samples with no detectable different traits, so that a panel of interaction partners is defined that distinguishes among previously indistinguishable samples. Those of ordinary skill in the art will understand, however, that the present invention often will allow both of these goals to be accomplished even in studies of sample collections with varying degrees of similarity and difference.

According to the present invention, interaction partners that bind to tumor samples may be characterized by their ability to discriminate among tumor samples. Any of a variety of techniques may be used to identify discriminating interaction partners. To give but one example, the present inventors have found it useful to define a "consensus panel" of tissue samples for tumors of a particular tissue of origin (see Examples 2-6). Those of ordinary skill in the art will again appreciate that the precise parameters used to designate a particular sample as interpretable and reproducible are not critical to the invention. Interaction partners may then be classified based on their ability to discriminate among tissue samples in the consensus panel (see Examples 2-6).

Assessing Prognosis or Therapeutic Regimen

The present invention further provides systems for identifying panels of interaction partners whose binding correlates with factors beyond tumor class or subclass, such as likelihood of a particular favorable or unfavorable outcome, susceptibility (or lack thereof) to a particular therapeutic regimen, etc.

As mentioned in the background, current approaches to assigning prognostic probabilities and/or selecting appropriate therapeutic regimens for particular tumors generally utilize the tumor-node-metastasis (TNM) system. This system uses the size of the tumor, the presence or absence of tumor in regional lymph nodes and the presence or absence of distant metastases, to assign a stage to the tumor. The assigned stage is used as a basis for selection of appropriate therapy and for prognostic purposes.

The present invention provides new methods and systems for evaluating tumor prognosis and/or recommended therapeutic approaches. In particular, the present invention provides systems for identifying panels of interaction partners whose binding correlates with tumor prognosis or therapeutic outcome.

For example, interaction partners whose binding correlates with prognosis can be identified by evaluating their binding to a collection of tumor samples for which prognosis is known or knowable. That is, the strategies of the invention may be employed either to identify collections of interaction partners whose binding correlates with a known outcome, or may be employed to identify a differential staining pattern that is then correlated with outcome (which outcome may either be known in advance or determined over time).

In general, it is preferred that inventive binding analyses be performed on human tumor samples. However, it is not necessary that the human tumors grow in a human host. Particularly for studies in which long-term outcome data are of interest (especially prognostic or predictive studies), it can be particularly useful to analyze samples grown in vitro (e.g., cell lines) or, more preferably, in a non-human host (e.g., a rodent, a dog, a sheep, a pig, or other animal). For instance, Example 9 provides a description of an assay in which inventive techniques employing human tumor cells growing in a non-human host are employed to define and/or utilize a panel of interaction partners whose binding to tumor samples correlates with prognosis and/or responsiveness to therapy.

It will often be desirable, when identifying interaction partners whose binding correlates with prognosis, to collect information about treatment regimens that may have been applied to the tumor whose sample is being assessed, in order to control for effects attributable to tumor therapy. Prognostic panel binding may correlate with outcome independent of treatment (Hayes et al., *J. Mamm. Gland Bio. Neo.* 6:375, 2001). Many prognostic markers, however, have both prognostic and predictive character (e.g., Her2/Neu status). Many of the individual interaction partners that comprise a prognostic panel may likewise have predictive capability and/or be members of a predictive panel.

Those of ordinary skill in the art will appreciate that prognostic panels (or individual interaction partners) have greater clinical utility if their binding/lack thereof correlates with positive/negative outcomes that are well separated statistically.

The inventive strategies may also be applied to the identification of predictive panels of interaction partners (i.e., panels whose binding correlates with susceptibility to a particular therapy). As noted above, some prognostic panels may also have predictive capabilities.

Interaction partners to be included in predictive panels are identified in binding studies performed on tumor samples that do or do not respond to a particular therapy. As with the prognostic panels, predictive panels may be assembled based on tests of tumor samples whose responsiveness is already known, or on samples whose responsiveness is not known in advance. As with the prognostic studies discussed above, the source of the tumor samples is not essential and can include, for example, tumor cell lines whose responsiveness to particular chemical agents has been determined, tumor samples from animal models in which tumors have been artificially introduced and therapeutic responsiveness has been determined and/or samples from naturally-occurring (human or other animal) tumors for which outcome data (e.g., time of survival, responsiveness to therapy, etc.) are available. Panels of interaction partners whose binding to tumor samples correlates with any prognostic or therapeutic trend can be defined and utilized as described herein.

Once correlations between interaction partner binding and tumor behavior have been established, the defined prognostic or predictive panels can be used to evaluate and classify tumor samples from patients and can be relied upon, for example to guide selection of an effective therapeutic regimen. As with the tumor classification studies described above, the process of identifying interaction partner panels whose binding correlates with outcome may itself identify particular outcomes not previously appreciated as distinct.

Those of ordinary skill in the art will appreciate that it is likely that, in at least some instances, tumor class or subclass identity will itself correlate with prognosis or responsiveness. In such circumstances, it is possible that the same set of interaction partners can act as both a classification panel and a prognosis or predictive panel.

Tumor Elements Bound By Interaction Partners

The inventive strategies for identifying and utilizing interaction partner panels in classifying or analyzing tumor samples do not rely on any assumptions about the identity or characteristics of the tumor components bound by the interaction partners. So long as interaction partner binding within the relevant panel correlates with some feature of interest, the

inventive teachings apply. In many if not most, cases, however, it is expected that binding will be with a protein expressed by tumor cells.

In some preferred embodiments of the invention, interaction partners bind to tumor markers that (a) are differentially expressed in tumor cells; (b) are members of protein families whose activities contribute to relevant biological events (e.g., gene families that have been implicated in cancer such as oncogenes, tumor suppressor genes, and genes that regulate apoptosis; gene families that have been implicated in drug resistance; etc.); (c) are present on or in the plasma membrane of the tumor cells; and/or (d) are the products of degradation of tumor components, which degradation products might be detectable in patient serum.

In fact, according to the present invention, interaction partners for analysis and use in inventive panels may sometimes be identified by first identifying a tumor-associated protein of interest, and then finding a potential interaction partner that binds with the protein. Binding by this potential interaction partner to tumor samples may then be assessed and utilized as described herein.

For example, as described in the Examples, the present inventors have successfully assembled classification panels comprised of antibodies that bind to tumor protein antigens. Candidate antigens were identified both through literature reviews of proteins that play a biological role in tumor initiation or progression, or that are known to be differentially expressed in tumors, and through gene expression studies that identified additional differentially expressed proteins.

Work by the present inventors, as well as by others, has already demonstrated that studies of gene expression patterns in large tumor cohorts can identify novel tumor classes (see, for example, Perou et al., *Nature* 406:747, 2000; Sorlie et al., *Proc Natl Acad. Sci. USA* 98:10869, 2001; van't Veer et al., *Nature* 415:530, 2002; West et al., *Proc Natl. Acad. Sci. USA* 98:11462, 2001; Hedenfalk et al., *N. Engl. J. Med.* 344:539, 2001; Gruvberger et al., *Cancer Res.* 61:5979, 2001; MacDonald et al., *Nature Genet.* 29:143, 2001; Pomeroy et al., *Nature* 415:436, 2002; Jazaeri et al., *J. Natl Cancer Inst* 94:990, 2002; Welsh et al., *Proc. Natl. Acad. Sci. USA* 98:1176, 2001; Wang et al., *Gene* 229:101, 1999; Beer et al., *Nature Med.* 8:816, 2002; Garber et al., *Proc Natl Acad Sci USA* 98:13784, 2001; Bhattacharjee et al., *Proc Natl Acad Sci USA* 98:13790, 2001; Zou et al., *Oncogene* 21:4855, 2002; Lin et al., *Oncogene* 21:4120, 2002; Alon et al., *Proc Natl Acad Sci USA* 96:6745, 1999; Takahashi et al., *Proc Natl Acad Sci USA* 98:9754, 2001; Singh et al., *Cancer Cell* 1:203, 2002; LaTulippe et al., *Cancer Res.* 62:4499, 2002; Welsh et al., *Cancer Res.* 61:5974, 2001; Dhanasekaran et al., *Nature* 412:822, 2001; Hippo et al., *Cancer Res.* 62:233, 2002; Yeoh et al., *Cancer Cell* 1:133, 2002; Hofmann et al., *Lancet* 359: 481, 2002; Ferrando et al., *Cancer Cell* 1:75, 2002; Shipp et al., *Nature Med* 8:68, 2002; Rosenwald et al., *N. Engl. J. Med.* 346:1937, 2002; and Alizadeh et al., *Nature* 403:503, 2000, each of which is incorporated herein by reference).

The gene sets described in these publications are promising candidates for genes that are likely to encode tumor markers whose interaction partners are useful in tumor classification and subclassification according to the present invention. Of particular interest are gene sets differentially expressed in solid tumors.

Furthermore, in general, given that differentially expressed genes are likely to be responsible for the different phenotypic characteristics of tumors, the present invention recognizes that such genes will often encode tumor markers for which a useful interaction partner, that discriminates among tumor classes or subclasses, can likely be prepared. A differentially expressed gene is a gene whose transcript abundance varies between different samples, e.g., between different tumor samples, between normal versus tumor samples, etc. In general, the amount by which the expression varies and the number of samples in which the expression varies by that amount will depend upon the number of samples and the particular characteristics of the samples. One skilled in the art will be able to determine, based on knowledge of the samples, what constitutes a significant degree of differential expression. Such genes can be identified by any of a variety of techniques including, for instance, in situ hybridization, Northern blot, nucleic acid amplification techniques (e.g., PCR, quantitative PCR, the ligase chain reaction, etc.), and, most commonly, microarray analysis.

Furthermore, those of ordinary skill in the art will readily appreciate, reading the present disclosure, that the inventive processes described herein of identifying and/or using sets of interaction partners whose binding (or lack thereof) correlates with an interesting tumor feature (e.g., tumor type or subtype, patient outcome, responsiveness of tumor or patient to therapy, etc.) inherently identifies both interaction partners of interest and the tumor markers to which they bind. Thus, one important aspect of the present invention is the identification of tumor markers whose ability (or lack thereof) to associate with an interaction partner correlates with a tumor characteristic of interest. Such tumor markers are useful as targets for identification of new therapeutic reagents, as well as of additional interaction partners useful in the practice of the present invention. Thus, it is to be understood that discussions of interaction partners presented herein are typically not limited to a particular interaction partner compound or entity, but may be generalized to include any compound or entity that binds to the relevant tumor marker(s) with requisite specificity and affinity.

Preparation of Interaction Partners

In general, interaction partners are entities that physically associate with selected tumor markers. Thus, any entity that binds detectably to a tumor marker may be utilized as an interaction partner in accordance with the present invention, so long as it binds with an appropriate combination of affinity and specificity.

Particularly preferred interaction partners are antibodies, or fragments (e.g., F(ab) fragments, $F(ab')_2$ fragments, Fv fragments, or sFv fragments, etc.; see, for example, Inbar et al., *Proc. Nat. Acad. Sci. USA* 69:2659, 1972; Hochman et al., *Biochem.* 15:2706, 1976; and Ehrlich et al., *Biochem.* 19:4091, 1980; Huston et al., *Proc. Nat. Acad. Sci. USA* 85:5879, 1998; U.S. Pat. Nos. 5,091,513 and 5,132,405 to Huston et al.; and U.S. Pat. No. 4,946,778 to Ladner et al., each of which is incorporated herein by reference). In certain embodiments, interaction partners may be selected from libraries of mutant antibodies (or fragments thereof). For example, collections of antibodies that each include different point mutations may be screened for their association with a tumor marker of interest. Yet further, chimeric antibodies may be used as interaction partners, e.g., "humanized" or "veneered" antibodies as described in greater detail below.

It is to be understood that the present invention is not limited to using antibodies or antibody fragments as interaction partners of inventive tumor markers. In particular, the present invention also encompasses the use of synthetic interaction partners that mimic the functions of antibodies. Several approaches to designing and/or identifying antibody mimics have been proposed and demonstrated (e.g., see the reviews by Hsieh-Wilson et al., *Acc. Chem. Res.* 29:164, 2000 and Peczuh and Hamilton, *Chem. Rev.* 100:2479, 2000). For example, small molecules that bind protein surfaces in a

fashion similar to that of natural proteins have been identified by screening synthetic libraries of small molecules or natural product isolates (e.g., see Gallop et al., *J. Med. Chem.* 37:1233, 1994; Gordon et al., *J. Med. Chem.* 37:1385, 1994; DeWitt et al., *Proc. Natl. Acad. Sci. U.S.A.* 90:6909, 1993; Bunin et al., *Proc. Natl. Acad. Sci. U.S.A.* 91:4708, 1994; Virgilio and Ellman, *J. Am. Chem. Soc.* 116:11580, 1994; Wang et al., *J. Med. Chem.* 38:2995, 1995; and Kick and Ellman, *J. Med. Chem.* 38:1427, 1995). Similarly, combinatorial approaches have been successfully applied to screen libraries of peptides and polypeptides for their ability to bind a range of proteins (e.g., see Cull et al., *Proc. Natl. Acad. Sci. U.S.A.* 89:1865, 1992; Mattheakis et al., *Proc. Natl. Acad. Sci. U.S.A.* 91:9022, 1994; Scott and Smith, *Science* 249:386, 1990; Devlin et al., *Science* 249:404, 1990; Corey et al., *Gene* 128:129, 1993; Bray et al., *Tetrahedron Lett.* 31:5811, 1990; Fodor et al., *Science* 251:767, 1991; Houghten et al., *Nature* 354:84, 1991; Lam et al., *Nature* 354:82, 1991; Blake and Litzi-Davis, *Bioconjugate Chem.* 3:510, 1992; Needels et al., *Proc. Natl. Acad. Sci. U.S.A.* 90:10700, 1993; and Ohlmeyer et al., *Proc. Natl. Acad. Sci. U.S.A.* 90:10922, 1993). Similar approaches have also been used to study carbohydrate-protein interactions (e.g., see Oldenburg et al., *Proc. Natl. Acad. Sci. U.S.A.* 89:5393, 1992) and polynucleotide-protein interactions (e.g., see Ellington and Szostak, *Nature* 346:818, 1990 and Tuerk and Gold, *Science* 249:505, 1990). These approaches have also been extended to study interactions between proteins and unnatural biopolymers such as oligocarbamates, oligoureas, oligosulfones, etc. (e.g., see Zuckermann et al., *J. Am. Chem. Soc.* 114:10646, 1992; Simon et al., *Proc. Natl. Acad. Sci. U.S.A.* 89:9367, 1992; Zuckermann et al., *J. Med. Chem.* 37:2678, 1994; Burgess et al., *Angew. Chem., Int. Ed. Engi.* 34:907, 1995; and Cho et al., *Science* 261:1303, 1993). Yet further, alternative protein scaffolds that are loosely based around the basic fold of antibody molecules have been suggested and may be used in the preparation of inventive interaction partners (e.g., see Ku and Schultz *Proc. Natl. Acad. Sci. U.S.A.* 92:6552, 1995). Antibody mimics comprising a scaffold of a small molecule such as 3-aminomethylbenzoic acid and a substituent consisting of a single peptide loop have also been constructed. The peptide loop performs the binding function in these mimics (e.g., see Smythe et al., *J. Am. Chem. Soc.* 116:2725, 1994). A synthetic antibody mimic comprising multiple peptide loops built around a calixarene unit has also been described (e.g., see U.S. Pat. No. 5,770,380 to Hamilton et al.).

Detecting Association of Interaction Partners and Tumor Markers

Any available strategy or system may be utilized to detect association between an interaction partner and its cognate tumor marker. In certain embodiments, association can be detected by adding a detectable label to the interaction partner. In other embodiments, association can be detected by using a labeled secondary interaction partner that associates specifically with the primary interaction partner, e.g., as is well known in the art of antigen/antibody detection. The detectable label may be directly detectable or indirectly detectable, e.g., through combined action with one or more additional members of a signal producing system. Examples of directly detectable labels include radioactive, paramagnetic, fluorescent, light scattering, absorptive and colorimetric labels. Examples of indirectly detectable include chemiluminescent labels, e.g., enzymes that are capable of converting a substrate to a chromogenic product such as alkaline phosphatase, horseradish peroxidase and the like.

Once a labeled interaction partner has bound a tumor marker, the complex may be visualized or detected in a variety of ways, with the particular manner of detection being chosen based on the particular detectable label, where representative detection means include, e.g., scintillation counting, autoradiography, measurement of paramagnetism, fluorescence measurement, light absorption measurement, measurement of light scattering and the like.

In general, association between an interaction partner and its cognate tumor marker may be assayed by contacting the interaction partner with a tumor sample that includes the marker. Depending upon the nature of the sample, appropriate methods include, but are not limited to, immunohistochemistry (IHC), radioimmunoassay, ELISA, immunoblotting and fluorescence activates cell sorting (FACS). In the case where the polypeptide is to be detected in a tissue sample, e.g., a biopsy sample, IHC is a particularly appropriate detection method. Techniques for obtaining tissue and cell samples and performing IHC and FACS are well known in the art.

The inventive strategies for classifying and/or subclassifying tumor samples may be applied to samples of any type and of any tissue of origin. In certain preferred embodiments of the invention, the strategies are applied to solid tumors. Historically, researchers have encountered difficulty in defining solid tumor subtypes, given the challenges associated with defining their molecular characteristics. As demonstrated in the Examples, the present invention is particularly beneficial in this area. Particularly preferred solid tumors include, for example, breast, lung, colon, and ovarian tumors. The invention also encompasses the recognition that tumor markers that are secreted from the cells in which they are produced may be present in serum, enabling their detection through a blood test rather than requiring a biopsy specimen. An interaction partner that binds to such tumor markers represents a particularly preferred embodiment of the invention.

In general, the results of such an assay can be presented in any of a variety of formats. The results can be presented in a qualitative fashion. For example, the test report may indicate only whether or not a particular tumor marker was detected, perhaps also with an indication of the limits of detection. Additionally the test report may indicate the subcellular location of binding, e.g., nuclear versus cytoplasmic and/or the relative levels of binding in these different subcellular locations. The results may be presented in a semi-quantitative fashion. For example, various ranges may be defined and the ranges may be assigned a score (e.g., 0 to 5) that provides a certain degree of quantitative information. Such a score may reflect various factors, e.g., the number of cells in which the tumor marker is detected, the intensity of the signal (which may indicate the level of expression of the tumor marker), etc. The results may be presented in a quantitative fashion, e.g., as a percentage of cells in which the tumor marker is detected, as a concentration, etc. As will be appreciated by one of ordinary skill in the art, the type of output provided by a test will vary depending upon the technical limitations of the test and the biological significance associated with detection of the tumor marker. For example, in the case of certain tumor markers a purely qualitative output (e.g., whether or not the tumor marker is detected at a certain detection level) provides significant information. In other cases a more quantitative output (e.g., a ratio of the level of expression of the tumor marker in two samples) is necessary.

Identification of Novel Therapies

Predictive panels of interaction agents are useful according to the present invention not only to classify tumor samples obtained from cancer sufferers with respect to their likely

responsiveness to known therapies, but also to identify potential new therapies or therapeutic agents that could be useful in the treatment of cancer.

For example, as noted above, the process of identifying or using inventive panels according to the present invention simultaneously identifies and/or characterizes tumor markers in or on the tumor cells that correlate with one or more selected tumor characteristics (e.g., tumor type or subtype, patient prognosis, and/or responsiveness of tumor or patient to therapy). Such tumor markers are attractive candidates for identification of new therapeutic agents (e.g., via screens to detect compounds or entities that bind to the tumor markers, preferably with at least a specified affinity and/or specificity, and/or via screens to detect compounds or entities that modulate (i.e., increase or decrease) expression, localization, modification, or activity of the tumor markers. In many instances, interaction partners themselves may prove to be useful therapeutics.

Thus the present invention provides interaction partners that are themselves useful therapeutic agents. For example, binding by an interaction partner, or a collection of interaction partners, to a cancer cell, might inhibit growth of that cell. Alternatively or additionally, interaction partners defined or prepared according to the present invention could be used to deliver a therapeutic agent to a cancer cell. In particular, interaction partners may be coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides and drugs. Preferred radionuclides include ^{90}Y, ^{123}I, ^{125}I, ^{131}I, ^{186}Re, ^{188}Re, ^{211}At and ^{212}Bi. Preferred drugs include chlorambucil, ifosphamide, mecloretharnine, cyclophosphamide, carboplatin, cisplatin, procarbazine, decarbazine, carmustine, cytarabine, hydroxyurea, mercaptopurine, methotrexate, thioguanine, 5-fluorouracil, actinomycin D, bleomycin, daunorubicin, doxorubicin, etoposide, vinblastine, vincristine, L-asparginase, adrenocorticosteroids, cancidovir triphosphate, adenine arabinonucleoside triphosphate, 5-aziridinyl-4-hydroxylamino-2-nitrobenzamide, acrolein, phosphoramide mustard, 6-methylpurine, etoposide, methotrexate, benzoic acid mustard, cyanide and nitrogen mustard.

According to such embodiments, the therapeutic agent may be coupled with an interaction partner by direct or indirect covalent or non-covalent interactions. A direct interaction between a therapeutic agent and an interaction partner is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (e.g., a halide) on the other. Indirect interactions might involve a linker group that is itself associated with both the therapeutic agent and the interaction partner. A linker group can function as a spacer to distance an interaction partner from an agent in order to avoid interference with association capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an interaction partner and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the catalog of the Pierce Chemical Co., Rockford, Ill.), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, e.g., U.S. Pat. No. 4,671,958, to Rodwell et al. It will further be appreciated that a therapeutic agent and an interaction partner may be coupled via non-covalent interactions, e.g., ligand/receptor type interactions. Any ligand/receptor pair with a sufficient stability and specificity to operate in the context of the invention may be employed to couple a therapeutic agent and an interaction partner. To give but an example, a therapeutic agent may be covalently linked with biotin and an interaction partner with avidin. The strong non-covalent binding of biotin to avidin would then allow for coupling of the therapeutic agent and the interaction partner. Typical ligand/receptor pairs include protein/co-factor and enzyme/substrate pairs. Besides the commonly used biotin/avidin pair, these include without limitation, biotin/streptavidin, digoxigenin/anti-digoxigenin, FK506/FK506-binding protein (FKBP), rapamycin/FKBP, cyclophilin/cyclosporin and glutathione/glutathione transferase pairs. Other suitable ligand/receptor pairs would be recognized by those skilled in the art, e.g., monoclonal antibodies paired with a epitope tag such as, without limitation, glutathione-S-transferase (GST), c-myc, FLAG® and maltose binding protein (MBP) and further those described in Kessler pp. 105-152 of *Advances in Mutagenesis"* Ed. by Kessler, Springer-Verlag, 1990*; "Affinity Chromatography: Methods and Protocols* (*Methods in Molecular Biology*)" Ed. by Pascal Baillon, Humana Press, 2000; and "*Immobilized Affinity Ligand Techniques"* by Hermanson et al., Academic Press, 1992.

Where a therapeutic agent is more potent when free from the interaction partner, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (e.g., U.S. Pat. No. 4,489,710 to Spitler), by irradiation of a photolabile bond (e.g., U.S. Pat. No. 4,625,014 to Senter et al.), by hydrolysis of derivatized amino acid side chains (e.g., U.S. Pat. No. 4,638,045 to Kohn et al.), by serum complement-mediated hydrolysis (e.g., U.S. Pat. No. 4,671,958 to Rodwell et al.) and by acid-catalyzed hydrolysis (e.g., U.S. Pat. No. 4,569,789 to Blattler et al.).

In certain embodiments, it may be desirable to couple more than one therapeutic agent to an interaction partner. In one embodiment, multiple molecules of an agent are coupled to one interaction partner molecule. In another embodiment, more than one type of therapeutic agent may be coupled to one interaction partner molecule. Regardless of the particular embodiment, preparations with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an interaction partner molecule, or linkers that provide multiple sites for attachment can be used.

Alternatively, a carrier can be used. A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (e.g., U.S. Pat. No. 4,507,234 to Kato et al.), peptides, and polysaccharides such as aminodextran (e.g., U.S. Pat. No. 4,699,784 to Shih et al.). A carrier may also bear an agent by non-covalent bonding or by encapsulation, such as within a liposome vesicle (e.g., U.S. Pat. Nos. 4,429,008 to Martin et al. and 4,873,088 to Mayhew et al.). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Pat. No. 4,735,792 to Srivastava discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing nitrogen and sulfur

atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Pat. No. 4,673,562 to Davison et al. discloses representative chelating compounds and their synthesis.

When interaction partners are themselves therapeutics, it will be understood that, in many cases, any interaction partner that binds with the same tumor marker may be so used.

In one preferred embodiment of the invention, the therapeutic agents (whether interaction partners or otherwise) are antibodies. As is well known in the art, when using an antibody or fragment thereof for therapeutic purposes it may prove advantageous to use a "humanized" or "veneered" version of an antibody of interest to reduce any potential immunogenic reaction. In general, "humanized" or "veneered" antibody molecules and fragments thereof minimize unwanted immunological responses toward antihuman antibody molecules which can limit the duration and effectiveness of therapeutic applications of those moieties in human recipients.

A number of "humanized" antibody molecules comprising an antigen binding portion derived from a non-human immunoglobulin have been described in the art, including chimeric antibodies having rodent variable regions and their associated complementarity-determining regions (CDRs) fused to human constant domains (e.g., see Winter et al., *Nature* 349: 293, 1991; Lobuglio et al., *Proc. Nat. Acad. Sci. USA* 86:4220, 1989; Shaw et al., *J. Immunol.* 138:4534, 1987; and Brown et al., *Cancer Res.* 47:3577, 1987), rodent CDRs grafted into a human supporting framework region (FR) prior to fusion with an appropriate human antibody constant domain (e.g., see Riechmann et al., *Nature* 332:323, 1988; Verhoeyen et al., *Science* 239:1534, 1988; and Jones et al. *Nature* 321:522, 1986) and rodent CDRs supported by recombinantly veneered rodent FRs (e.g., see European Patent Publication No. 519,596, published Dec. 23, 1992). It is to be understood that the invention also encompasses "fully human" antibodies produced using the XenoMouse™ technology (AbGenix Corp., Fremont, Calif.) according to the techniques described in U.S. Pat. No. 6,075,181.

Yet further, so-called "veneered" antibodies may be used that include "veneered FRs". The process of veneering involves selectively replacing FR residues from, e.g., a murine heavy or light chain variable region, with human FR residues in order to provide a xenogeneic molecule comprising an antigen binding portion which retains substantially all of the native FR polypeptide folding structure. Veneering techniques are based on the understanding that the antigen binding characteristics of an antigen binding portion are determined primarily by the structure and relative disposition of the heavy and light chain CDR sets within the antigen-association surface (e.g., see Davies et al., *Ann. Rev. Biochem.* 59:439, 1990). Thus, antigen association specificity can be preserved in a humanized antibody only wherein the CDR structures, their interaction with each other and their interaction with the rest of the variable region domains are carefully maintained. By using veneering techniques, exterior (e.g., solvent-accessible) FR residues which are readily encountered by the immune system are selectively replaced with human residues to provide a hybrid molecule that comprises either a weakly immunogenic, or substantially non-immunogenic veneered surface.

Preferably, interaction partners suitable for use as therapeutics (or therapeutic agent carriers) exhibit high specificity for the target tumor marker and low background binding to other tumor markers. In certain embodiments, monoclonal antibodies are preferred for therapeutic purposes.

Tumor markers that are expressed on the cell surface represent preferred targets for the development of therapeutic agents, particularly therapeutic antibodies. For example, cell surface proteins can be tentatively identified using sequence analysis based on the presence of a predicted transmembrane domain. Their presence on the cell surface can ultimately be confirmed using IHC.

Kits

Useful sets or panels of interaction partners according to the present invention may be prepared and packaged together in kits for use in classifying, diagnosing, or otherwise characterizing tumor samples, or for inhibiting tumor cell growth or otherwise treating cancer.

Any available technique may be utilized in the preparation of individual interaction partners for inclusion in kits. For example, protein or polypeptide interaction partners may be produced by cells (e.g., recombinantly or otherwise), may be chemically synthesized, or may be otherwise generated in vitro (e.g., via in vitro transcription and/or translation). Non-protein or polypeptide interaction partners (e.g., small molecules, etc.) may be synthesized, may be isolated from within or around cells that produce them, or may be otherwise generated.

When antibodies are used as interaction partners, these may be prepared by any of a variety of techniques known to those of ordinary skill in the art (e.g., see Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988). For example, antibodies can be produced by cell culture techniques, including the generation of monoclonal antibodies, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies. In one technique, an "immunogen" comprising an antigenic portion of a tumor marker of interest (or the tumor marker itself) is initially injected into any of a wide variety of mammals (e.g., mice, rats, rabbits, sheep or goats). In this step, a tumor marker (or an antigenic portion thereof) may serve as the immunogen without modification. Alternatively, particularly for relatively short tumor markers, a superior immune response may be elicited if the tumor marker is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin (KLH). The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations and the animals are bled periodically. Polyclonal antibodies specific for the tumor marker may then be purified from such antisera by, for example, affinity chromatography using the tumor marker (or an antigenic portion thereof) coupled to a suitable solid support. An exemplary method is described in Example 7.

If desired for diagnostic or therapeutic kits, monoclonal antibodies specific for a tumor marker of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511, 1976 and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (i.e., reactivity with the tumor marker of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection

technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and their culture supernatants tested for binding activity against the tumor marker. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation and extraction. The tumor marker of interest may be used in the purification process in, for example, an affinity chromatography step.

In addition to inventive interaction partners, preferred kits for use in accordance with the present invention may include, a reference sample, instructions for processing samples, performing the test, instructions for interpreting the results, buffers and/or other reagents necessary for performing the test. In certain embodiments the kit can comprise a panel of antibodies.

Pharmaceutical Compositions

As mentioned above, the present invention provides new therapies and methods for identifying these. In certain embodiments, an interaction partner may be a useful therapeutic agent. Alternatively or additionally, interaction partners defined or prepared according to the present invention bind to tumor markers that serve as targets for therapeutic agents. Also, inventive interaction partners may be used to deliver a therapeutic agent to a cancer cell. For example, interaction partners provided in accordance with the present invention may be coupled to one or more therapeutic agents.

In addition, as mentioned above, to the extent that a particular predictive panel correlates with responsiveness to a particular therapy because it detects changes that reflect inhibition (or inhibitability) of cancer cell growth, that panel could be used to evaluate therapeutic candidates (e.g., small molecule drugs) for their ability to induce the same or similar changes in different cells. In particular, binding by the panel could be assessed on cancer cells before and after exposure to candidate therapeutics; those candidates that induce expression of the tumor markers to which the panel binds are then identified.

The invention includes pharmaceutical compositions comprising these inventive therapeutic agents. In general, a pharmaceutical composition will include a therapeutic agent in addition to one or more inactive agents such as a sterile, biocompatible carrier including, but not limited to, sterile water, saline, buffered saline, or dextrose solution. The pharmaceutical compositions may be administered either alone or in combination with other therapeutic agents including other chemotherapeutic agents, hormones, vaccines and/or radiation therapy. By "in combination with", it is not intended to imply that the agents must be administered at the same time or formulated for delivery together, although these methods of delivery are within the scope of the invention. In general, each agent will be administered at a dose and on a time schedule determined for that agent. Additionally, the invention encompasses the delivery of the inventive pharmaceutical compositions in combination with agents that may improve their bioavailability, reduce or modify their metabolism, inhibit their excretion, or modify their distribution within the body. The invention encompasses treating cancer by administering the pharmaceutical compositions of the invention. Although the pharmaceutical compositions of the present invention can be used for treatment of any subject (e.g., any animal) in need thereof, they are most preferably used in the treatment of humans.

The pharmaceutical compositions of this invention can be administered to humans and other animals by a variety of routes including oral, intravenous, intramuscular, intra-arterial, subcutaneous, intraventricular, transdermal, rectal, intravaginal, intraperitoneal, topical (as by powders, ointments, or drops), bucal, or as an oral or nasal spray or aerosol. In general the most appropriate route of administration will depend upon a variety of factors including the nature of the agent (e.g., its stability in the environment of the gastrointestinal tract), the condition of the patient (e.g., whether the patient is able to tolerate oral administration), etc. At present the intravenous route is most commonly used to deliver therapeutic antibodies. However, the invention encompasses the delivery of the inventive pharmaceutical composition by any appropriate route taking into consideration likely advances in the sciences of drug delivery.

General considerations in the formulation and manufacture of pharmaceutical agents may be found, for example, in *Remington's Pharmaceutical Sciences,* 19th ed., Mack Publishing Co., Easton, Pa., 1995.

According to the methods of treatment of the present invention, cancer is treated or prevented in a patient such as a human or other mammal by administering to the patient a therapeutically effective amount of a therapeutic agent of the invention, in such amounts and for such time as is necessary to achieve the desired result. By a "therapeutically effective amount" of a therapeutic agent of the invention is meant a sufficient amount of the therapeutic agent to treat (e.g., to ameliorate the symptoms of, delay progression of, prevent recurrence of, cure, etc.) cancer at a reasonable benefit/risk ratio, which involves a balancing of the efficacy and toxicity of the therapeutic agent. In general, therapeutic efficacy and toxicity may be determined by standard pharmacological procedures in cell cultures or with experimental animals, e.g., by calculating the ED_{50} (the dose that is therapeutically effective in 50% of the treated subjects) and the LD_{50} (the dose that is lethal to 50% of treated subjects). The ED_{50}/LD_{50} represents the therapeutic index of the agent. Although in general therapeutic agents having a large therapeutic index are preferred, as is well known in the art, a smaller therapeutic index may be acceptable in the case of a serious disease, particularly in the absence of alternative therapeutic options. Ultimate selection of an appropriate range of doses for administration to humans is determined in the course of clinical trials.

It will be understood that the total daily usage of the therapeutic agents and compositions of the present invention for any given patient will be decided by the attending physician within the scope of sound medical judgment. The specific therapeutically effective dose level for any particular patient will depend upon a variety of factors including the disorder being treated and the severity of the disorder; the activity of the specific therapeutic agent employed; the specific composition employed; the age, body weight, general health, sex and diet of the patient; the time of administration, route of administration and rate of excretion of the specific therapeutic agent employed; the duration of the treatment; drugs used in combination or coincidental with the specific therapeutic agent employed; and like factors well known in the medical arts.

The total daily dose of the therapeutic agents of this invention administered to a human or other mammal in single or in divided doses can be in amounts, for example, from 0.01 to 50 mg/kg body weight or more usually from 0.1 to 25 mg/kg

body weight. Single dose compositions may contain such amounts or submultiples thereof to make up the daily dose. In general, treatment regimens according to the present invention comprise administration to a patient in need of such treatment from about 0.1 μg to about 2000 mg of the therapeutic agent(s) of the invention per day in single or multiple doses.

EXEMPLIFICATION

Example 1

Selection of Candidate Genes and Identification of Potential Interaction Partners for Tumor Classification Panels

The present inventors identified a collection of candidate genes that (a) were differentially expressed across a set of tumor samples in a manner that suggested they distinguish biologically distinct classes of tumors; (b) were members of a gene functional class that has been linked to cellular pathways implicated in tumor prognosis or drug resistance; (c) were known or thought to display an expression, localization, modification, or activity pattern that correlates with a relevant tumor feature; etc.

For example, differentially expressed genes were identified using microarrays as described in co-pending U.S. patent application Ser. No. 09/916,722, filed Jul. 26, 2001 entitled "REAGENTS AND METHODS FOR USE IN MANAGING BREAST CANCER", the entire contents of which are incorporated herein by reference. Other genes were typically selected on the basis of published data suggesting their possible implication in drug resistance, cancer prognosis, etc. A total of 730 candidate genes were identified as encoding proteins against which antibodies should be raised.

Rabbit polyclonal affinity-purified antibodies were then raised against 661 of these proteins as described in Example 7. Each antibody was initially tested over a range of dilutions on tissue arrays that included a set of normal tissues, tumor tissues and cell lines, so that, for each antibody, a discriminating titer was established at which differential staining across the diverse set was observed. The preparation and staining of tissue arrays is described in greater detail in Example 8. Of the 661 antibodies subjected to this analysis, 460 showed differential staining and were considered of sufficient interest for further analysis.

Example 2

Breast Cancer Classification Panel (Russian Breast Cohort)

The present inventors prepared an exemplary panel of antibodies for use in classifying breast tumors. 272 of the 460 differentially staining antibodies of Example 1 exhibited a reproducibly robust staining pattern on tissues relevant for this application. These antibodies were therefore applied (at appropriate titers) to a tissue array comprised of approximately 400 independent breast tumor samples from a cohort of breast cancer patients (the Russian breast cohort). Stained tissue samples were scored by a trained cytotechnologist or pathologist on a semi-quantitative scale in which 0=no stain on tumor cells; 1=no information; 2=weak staining of tumor cells; and 3=strong staining of tumor cells. Antibodies were included in a breast cancer classification panel if they stained greater than 10% and less than 90% of a defined "consensus panel" of the breast tumor tissue samples on at least two independent tissue arrays.

A given tissue sample was included in this "consensus panel" if at least 80% of the antibodies tested gave interpretable scores (i.e., a non-zero score) with that sample. Of the 400 breast tumor samples in the tissue array about 320 were included in the consensus panel. Also, in scoring antibody binding to the consensus panel, all scores represented a consensus score of replicate tissue arrays comprised of independent samples from the same sources. The consensus score was determined by computing the median (rounded down to an integer, where applicable) of all scores associated with a given antibody applied under identical conditions to the particular patient sample. In cases where the variance of the scores was greater than 2, the score was changed to 1 (i.e., no information). The data for each antibody was stored in an Oracle-based database that contained the semi-quantitative scores of tumor tissue staining and also contained links to both patient clinical information and stored images of the stained patient samples.

Through this analysis 90 of the 272 tested antibodies were selected for inclusion in an exemplary breast cancer classification panel (see Appendix A, e.g., S0021, S0022, S0039, etc.). It is to be understood that any sub-combination of these 90 antibodies may be used in constructing an inventive breast cancer classification panel. It will also be appreciated that additional antibodies may be added to or removed from an inventive breast cancer classification panel as more tumor markers are identified and/or more samples are tested (e.g., see Example 3).

FIG. **1** shows the pattern of reactivity observed with certain members of this panel of antibodies across samples from the Russian breast cohort. Dark gray represents strong positive staining, black represents weak positive staining, while light gray represents the absence of staining and medium gray represents a lack of data. Images of stained samples can be found in Appendix B (see right hand column of Appendix A for cross-references to corresponding antibodies).

The patients (rows) were classified using k-means clustering (as described, for example, in MacQueen in *Proceedings of the Fifth Berkeley Symposium on Mathematical Statistics and Probability* (Le Cam et al., Eds.; University of California Press, Berkeley, Calif.) 1:281, 1967; Heyer et al., *Genome Res.* 9:1106, 1999, each of which is incorporated herein by reference) while the antibodies (columns) were organized using hierarchical clustering (as described in, for example, Sokal et al., *Principles of Numerical Tazonomy* (Freeman & Co., San Francisco, Calif.), 1963; Eisen et al., *Proc. Natl. Acad. Sci. USA* 95:14863, 1998, each of which is incorporated herein by reference). As shown in FIG. **1**, nine subclasses of breast cancer patients were identified by their consensus pattern of staining with this breast cancer classification panel.

Example 3

Breast Cancer Classification Panel (HH Breast Cohort)

In order to refine and expand the breast cancer classification panel of Example 2, the present inventors tested 109 of the 460 differentially staining antibodies of Example 1 on samples from a new cohort of 550 breast cancer patients (the Huntsville Hospital breast cohort or "HH breast" cohort, the characteristics of which are described in Example 10).

Antibodies were included in an updated breast cancer classification panel if they stained more than 10% and less than 90% of the particular consensus panel of tissue samples tested. Through this analysis 87 of the 109 tested antibodies were selected (see Appendix A, e.g., S0011, S0018, S0020, etc.).

Example 4

Lung Cancer Classification Panel (Russian Lung Cohort)

The present inventors also prepared an exemplary panel of antibodies for use in classifying lung tumors. 417 of the 460 differentially staining antibodies of Example 1 exhibited a reproducibly robust staining pattern on tissues relevant for this application. These antibodies were therefore applied (at the titers determined in Example 1) to a tissue array comprised of approximately 400 independent lung tumor tissues from a cohort of lung cancer patients (the Russian lung cohort). Stained tissue samples were scored by a trained cytotechnologist or pathologist as before and again antibodies were included in the classification panel if they stained greater than 10% and less than 90% of a defined "consensus panel" of tissue samples on at least two independent tissue arrays.

Through this analysis an exemplary lung cancer classification panel was generated that was made up of 106 of the 417 tested antibodies (see Appendix A, e.g., s0021, s0022, s0024, etc.). It is to be understood that any sub-combination of these 106 antibodies may be used in constructing an inventive lung cancer classification panel. It will also be appreciated that additional antibodies may be added to or removed from an inventive lung cancer classification panel as more tumor markers are identified and/or more samples are tested (e.g., see Example 5).

FIG. **2** shows the pattern of reactivity observed with certain members of this panel of antibodies across samples from the Russian lung cohort. Dark gray represents strong positive staining, black represents weak positive staining, while light gray represents the absence of staining and medium gray represents a lack of data. Images of stained samples can be found in Appendix B (see right hand column of Appendix A for cross-references to corresponding antibodies).

The patients (rows) were again classified using k-means clustering while the antibodies (columns) were organized using hierarchical clustering. As shown in FIG. **2**, eight subclasses of lung cancer patients were identified by their consensus pattern of staining with this lung cancer classification panel.

Example 5

Lung Cancer Classification Panel (HH Lung Cohort)

In order to refine and expand the lung cancer classification panel of Example 4, the present inventors tested 54 of the 460 differentially staining antibodies of Example 1 on samples from a new cohort of 379 lung cancer patients (the Huntsville Hospital lung cohort or "HH lung" cohort, the characteristics of which are described in Example 11).

Antibodies were included in an updated colon cancer classification panel if they stained more than 10% and less than 90% of the particular consensus panel of tissue samples tested. Through this analysis 39 of the 54 tested antibodies were selected (see Appendix A, e.g., S0021, S0022, S0046, etc.).

Example 6

Colon Cancer Classification Panel (Russian Colon Cohort)

The present inventors also prepared an exemplary panel of antibodies for use in classifying colon tumors. 382 of the 460 differentially staining antibodies of Example 1 exhibited a reproducibly robust staining pattern on tissues relevant for this application. These antibodies were therefore applied (at the titers determined in Example 1) to a tissue array comprised of approximately 400 independent colon tumor tissues from a cohort of colon cancer patients (the Russian colon cohort). Stained tissue samples were scored by a trained cytotechnologist or pathologist as before and again antibodies were included in the classification panel if they stained greater than 10% and less than 90% of a defined "consensus panel" of tissue samples on at least two independent tissue arrays.

Through this analysis a colon antibody classification panel was generated that was made up of 86 of the 382 tested antibodies (see Appendix A, e.g., S0022, S0036, S0039, etc.). It will be appreciated that any sub-combination of these 86 antibodies may be used in constructing an inventive colon cancer classification panel. It will also be appreciated that additional antibodies may be added to or removed from an inventive colon cancer classification panel as more tumor markers are identified and/or more samples are tested.

FIG. **3** shows the pattern of reactivity observed with certain members of this panel of antibodies across samples from the Russian colon cohort. Dark gray represents strong positive staining, black represents weak positive staining, while light gray represents the absence of staining and medium gray represents a lack of data. Images of the stained samples can be found in Appendix B (see right hand column of Appendix A for cross-references to corresponding antibodies).

The patients (rows) were again classified using k-means clustering while the antibodies (columns) were organized using hierarchical clustering. As shown in FIG. **3**, seven subclasses of patients were identified by their consensus pattern of staining with this exemplary colon cancer classification panel.

Example 7

Raising Antibodies

This example describes a method that was employed to generate the majority of the antibodies that were used in Examples 1-6. Similar methods may be used to generate an antibody that binds to any polypeptide of interest (e.g., to polypeptides that are or are derived from other tumor markers). In some cases, antibodies may be obtained from commercial sources (e.g., Chemicon, Dako, Oncogene Research Products, NeoMarkers, etc.) or other publicly available sources (e.g., Imperial Cancer Research Technology, etc.).

Materials and Solutions

Anisole (Cat. No. A4405, Sigma, St. Louis, Mo.)

2,2'-azino-di-(3-ethyl-benzthiazoline-sulfonic acid) (ABTS) (Cat. No. A6499, Molecular Probes, Eugene, Oreg.)

Activated maleimide Keyhole Limpet Hemocyanin (Cat. No. 77106, Pierce, Rockford, Ill.)

Keyhole Limpet Hemocyanin (Cat. No. 77600, Pierce, Rockford, Ill.)

Phosphoric Acid (H_3PO_4) (Cat. No. P6560, Sigma)

Glacial Acetic Acid (Cat No. BP1185-500, Fisher)

EDC (EDAC) (Cat No. 341006, Calbiochem)
25% Glutaraldehyde (Cat No. G-5882, Sigma)
Glycine (Cat No. G-8898, Sigma)
Biotin (Cat. No. B2643, Sigma)
Boric acid (Cat. No. B0252, Sigma)
Sepharose 4B (Cat. No. 17-0120-01, LKB/Pharmacia, Uppsala, Sweden)
Bovine Serum Albumin (LP) (Cat. No. 100 350, Boehringer Mannheim, Indianapolis, Ind.)
Cyanogen bromide (Cat. No. C6388, Sigma)
Dialysis tubing Spectra/Por Membrane MWCO: 6-8,000 (Cat. No. 132 665, Spectrum Industries, Laguna Hills, Calif.)
Dimethyl formamide (DMF) (Cat. No. 22705-6, Aldrich, Milwaukee, Wis.)
DIC (Cat. No. BP 592-500, Fisher)
Ethanedithiol (Cat. No. 39, 802-0, Aldrich)
Ether (Cat. No. TX 1275-3, EM Sciences)
Ethylenediaminetetraacetatic acid (EDTA) (Cat. No. BP 120-1, Fisher, Springfield, N.J.)
1-ethyl-3-(3' dimethylaminopropyl)-carbodiimide, HCL (EDC) (Cat. no. 341-006, Calbiochem, San Diego, Calif.)
Freund's Adjuvant, complete (Cat. No. M-0638-50B, Lee Laboratories, Grayson, Ga.)
Freund's Adjuvant, incomplete (Cat. No. M-0639-50B, Lee Laboratories)
Fritted chromatography columns (Column part No. 12131011; Frit Part No. 12131029, Varian Sample Preparation Products, Harbor City, Calif.)
Gelatin from Bovine Skin (Cat. No. G9382, Sigma)
Goat anti-rabbit IgG, biotinylated (Cat. No. A 0418, Sigma)
HOBt (Cat. No. 01-62-0008, Calbiochem)
Horseradish peroxidase (HRP) (Cat. No. 814 393, Boehringer Mannheim)
HRP-Streptavidin (Cat. No. S 5512, Sigma)
Hydrochloric Acid (Cat. No. 71445-500, Fisher)
Hydrogen Peroxide 30% w/w (Cat. No. H1009, Sigma)
Methanol (Cat. No. A412-20, Fisher)
Microtiter plates, 96 well (Cat. No. 2595, Corning-Costar, Pleasanton, Calif.)
N-α-Fmoc protected amino acids from Calbiochem. See '97-'98 Catalog pp. 1-45.
N-α-Fmoc protected amino acids attached to Wang Resin from Calbiochem. See '97-'98 Catalog pp. 161-164.
NMP (Cat. No. CAS 872-50-4, Burdick and Jackson, Muskegon, Mich.)
Peptide (Synthesized by Research Genetics. Details given below)
Piperidine (Cat. No. 80640, Fluka, available through Sigma)
Sodium Bicarbonate (Cat. No. BP328-1, Fisher)
Sodium Borate (Cat. No. B9876, Sigma)
Sodium Carbonate (Cat. No. BP357-1, Fisher)
Sodium Chloride (Cat. No. BP 358-10, Fisher)
Sodium Hydroxide (Cat. No. SS 255-1, Fisher)
Streptavidin (Cat. No. 1 520, Boehringer Mannheim)
Thioanisole (Cat. No. T-2765, Sigma)
Trifluoroacetic acid (Cat. No. TX 1275-3, EM Sciences)
Tween-20 (Cat. No. BP 337-500, Fisher)
Wetbox (Rectangular Servin' Saver™ Part No. 3862, Rubbermaid, Wooster, Ohio)
BBS—Borate Buffered Saline with EDTA dissolved in distilled water (pH 8.2 to 8.4 with HCl or NaOH), 25 mM Sodium borate (Borax), 100 mM Boric Acid, 75 mM NaCl and 5 mM EDTA.
0.1 N HCl in saline as follows: concentrated HCl (8.3 ml/0.917 liter distilled water) and 0.154 M NaCl
Glycine (pH 2.0 and pH 3.0) dissolved in distilled water and adjusted to the desired pH, 0.1 M glycine and 0.154 M NaCl.
5× Borate 1× Sodium Chloride dissolved in distilled water, 0.11 M NaCl, 60 mM Sodium Borate and 250 mM Boric Acid.
Substrate Buffer in distilled water adjusted to pH 4.0 with sodium hydroxide, 50 to 100 mM Citric Acid.
AA solution: HOBt is dissolved in NMP (8.8 grams HOBt to 1 liter NMP). Fmoc-N-a-amino at a concentration at 0.53 M.
DIC solution: 1 part DIC to 3 parts NMP.
Deprotecting solution: 1 part Piperidine to 3 parts DMF.
Reagent R: 2 parts anisole, 3 parts ethanedithiol, 5 parts thioanisole and 90 parts trifluoroacetic acid.

Equipment

MRX Plate Reader (Dynatech, Chantilly, Va.)
Hamilton Eclipse (Hamilton Instruments, Reno, Nev.)
Beckman TJ-6 Centrifuge (Model No. TJ-6, Beckman Instruments, Fullerton, Calif.)
Chart Recorder (Recorder 1 Part No. 18-1001-40, Pharmacia LKB Biotechnology)
UV Monitor (Uvicord SU Part No. 18-1004-50, Pharmacia LKB Biotechnology)
Amicon Stirred Cell Concentrator (Model 8400, Amicon, Beverly, Mass.)
30 kD MW cut-off filter (Cat. No. YM-30 Membranes Cat. No. 13742, Amicon)
Multi-channel Automated Pipettor (Cat. No. 4880, Corning Costar, Cambridge, Mass.)
pH Meter Corning 240 (Corning Science Products, Corning Glassworks, Corning, N.Y.)
ACT396 peptide synthesizer (Advanced ChemTech, Louisville, Ky.)
Vacuum dryer (Box from Labconco, Kansas City, Mo. and Pump from Alcatel, Laurel, Md.).
Lyophilizer (Unitop 600s1 in tandem with Freezemobile 12, both from Virtis, Gardiner, N.Y.)

Peptide Selection

Peptides against which antibodies would be raised were selected from within the polypeptide sequence of interest using a program that uses the Hopp/Woods method (described in Hopp and Woods, *Mol. Immunol.* 20:483, 1983 and Hopp and Woods, *Proc. Nat. Acad. Sci. U.S.A.* 78:3824, 1981). The program uses a scanning window that identifies peptide sequences of 15-20 amino acids containing several putative antigenic epitopes as predicted by low solvent accessibility. This is in contrast to most implementations of the Hopp/Woods method, which identify single short (~6 amino acids) presumptive antigenic epitopes. Occasionally the predicted solvent accessibility was further assessed by PHD prediction of loop structures (described in Rost and Sander, *Proteins* 20:216, 1994). Preferred peptide sequences display minimal similarity with additional known human proteins. Similarity was determined by performing BLASTP alignments, using a wordsize of 2 (described in Altschul et al., *J. Mol. Biol.* 215:403, 1990). All alignments given an EXPECT value less than 1000 were examined and alignments with similarities of greater than 60% or more than four residues in an exact contiguous non-gapped alignment forced those peptides to be rejected. When it was desired to target regions of proteins exposed outside the cell membrane, extracellular regions of the protein of interest were determined from the literature or as defined by predicted transmembrane domains using a hidden Markov model (described in Krogh et al., *J.*

Mol. Biol. 305:567, 2001). When the peptide sequence was in an extracellular domain, peptides were rejected if they contained N-linked glycosylation sites. As shown in Appendix A, one to three peptide sequences were selected for each polypeptide using this procedure.

Peptide Synthesis

The sequence of the desired peptide was provided to the peptide synthesizer. The C-terminal residue was determined and the appropriate Wang Resin was attached to the reaction vessel. The peptides were synthesized C-terminus to N-terminus by adding one amino acid at a time using a synthesis cycle. Which amino acid is added was controlled by the peptide synthesizer, which looks to the sequence of the peptide that was entered into its database. The synthesis steps were performed as follows:

Step 1—Resin Swelling: Added 2 ml DMF, incubated 30 minutes, drained DMF.

Step 2—Synthesis cycle (repeated over the length of the peptide)

2a—Deprotection: 1 ml deprotecting solution was added to the reaction vessel and incubated for 20 minutes.

2b—Wash Cycle

2c—Coupling: 750 ml of amino acid solution (changed as the sequence listed in the peptide synthesizer dictated) and 250 ml of DIC solution were added to the reaction vessel. The reaction vessel was incubated for thirty minutes and washed once. The coupling step was repeated once.

2d—Wash Cycle

Step 3—Final Deprotection: Steps 2a and 2b were performed one last time.

Resins were deswelled in methanol (rinsed twice in 5 ml methanol, incubated 5 minutes in 5 ml methanol, rinsed in 5 ml methanol) and then vacuum dried.

Peptide was removed from the resin by incubating 2 hours in reagent R and then precipitated into ether. Peptide was washed in ether and then vacuum dried. Peptide was resolubilized in diH_2O, frozen and lyophilized overnight.

Conjugation of Peptide with Keyhole Limpet Hemocyanin

Peptide (6 mg) was conjugated with Keyhole Limpet Hemocyanin (KLH). When the selected peptide included at least one cysteine, three aliquots (2 mg) were dissolved in PBS (2 ml) and coupled to KLH via glutaraldehyde, EDC or maleimide activated KLH (2 mg) in 2 ml of PBS for a total volume of 4 ml. When the peptide lacked cysteine, two aliquots (3 mg) were coupled via glutaraldehyde and EDC methods.

Maleimide coupling is accomplished by mixing 2 mg of peptide with 2 mg of maleimide-activated KLH dissolved in PBS (4 ml) and incubating 4 hr.

EDC coupling is accomplished by mixing 2 mg of peptide, 2 mg unmodified KLH, and 20 mg of EDC in 4 ml PBS (lowered to pH 5 by the addition of phosphoric acid), and incubating for 4 hours. The reaction is stopped by the slow addition of 1.33 ml acetic acid (pH 4.2). When using EDC to couple 3 mg of peptide, the amounts listed above are increased by a factor of 1.5.

Glutaraldehyde coupling occurs when 2 mg of peptide are mixed with 2 mg of KLH in 0.9 ml of PBS. 0.9 ml of 0.2% glutaraldehyde in PBS is added and mixed for one hour. 0.46 ml of 1 M glycine in PBS is added and mixed for one hour. When using glutaraldehyde to couple 3 mg of peptide, the above amounts are increased by a factor of 1.5.

The conjugated aliquots were subsequently repooled, mixed for two hours, dialyzed in 1 liter PBS and lyophilized.

Immunization of Rabbits

Two New Zealand White Rabbits were injected with 250 μg (total) KLH conjugated peptide in an equal volume of complete Freund's adjuvant and saline in a total volume of 1 ml. 100 μg KLH conjugated peptide in an equal volume of incomplete Freund's Adjuvant and saline were then injected into three to four subcutaneous dorsal sites for a total volume of 1 ml two, six, eight and twelve weeks after the first immunization. The immunization schedule was as follows:

Day 0	Pre-immune bleed, primary immunization
Day 15	1st boost
Day 27	1st bleed
Day 44	2nd boost
Day 57	2nd bleed and 3rd boost
Day 69	3rd bleed
Day 84	4th boost
Day 98	4th bleed

Collection of Rabbit Serum

The rabbits were bled (30 to 50 ml) from the auricular artery. The blood was allowed to clot at room temperature for 15 minutes and the serum was separated from the clot using an IEC DPR-6000 centrifuge at 5000 g. Cell-free serum was decanted gently into a clean test tube and stored at −20° C. for affinity purification.

Determination of Antibody Titer

All solutions with the exception of wash solution were added by the Hamilton Eclipse, a liquid handling dispenser. The antibody titer was determined in the rabbits using an ELISA assay with peptide on the solid phase. Flexible high binding ELISA plates were passively coated with peptide diluted in BBS (100 μl, 1 μg/well) and the plate was incubated at 4° C. in a wetbox overnight (air-tight container with moistened cotton balls). The plates were emptied and then washed three times with BBS containing 0.1% Tween-20 (BBS-TW) by repeated filling and emptying using a semi-automated plate washer. The plates were blocked by completely filling each well with BBS-TW containing 1% BSA and 0.1% gelatin (BBS-TW-BG) and incubating for 2 hours at room temperature. The plates were emptied and sera of both pre- and post-immune serum were added to wells. The first well contained sera at 1:50 in BBS. The sera were then serially titrated eleven more times across the plate at a ratio of 1:1 for a final (twelfth) dilution of 1:204,800. The plates were incubated overnight at 4° C. The plates were emptied and washed three times as described.

Biotinylated goat anti-rabbit IgG (100 μl) was added to each microtiter plate test well and incubated for four hours at room temperature. The plates were emptied and washed three times. Horseradish peroxidase-conjugated Streptavidin (100 μl diluted 1:10,000 in BBS-TW-BG) was added to each well and incubated for two hours at room temperature. The plates were emptied and washed three times. The ABTS was prepared fresh from stock by combining 10 ml of citrate buffer (0.1 M at pH 4.0), 0.2 ml of the stock solution (15 mg/ml in water) and 10 μl of 30% hydrogen peroxide. The ABTS solution (100 μl) was added to each well and incubated at room temperature. The plates were read at 414 nm, 20 minutes following the addition of substrate.

Preparation of Peptide Affinity Purification Column:

The affinity column was prepared by conjugating 5 mg of peptide to 10 ml of cyanogen bromide-activated Sepharose 4B and 5 mg of peptide to hydrazine-Sepharose 4B. Briefly, 100 μl of DMF was added to peptide (5 mg) and the mixture was vortexed until the contents were completely wetted. Water was then added (900 μl) and the contents were vortexed

until the peptide dissolved. Half of the dissolved peptide (500 μl) was added to separate tubes containing 10 ml of cyanogen-bromide activated Sepharose 4B in 0.1 ml of borate buffered saline at pH 8.4 (BBS) and 10 ml of hydrazine-Sepharose 4B in 0.1 M carbonate buffer adjusted to pH 4.5 using excess EDC in citrate buffer pH 6.0. The conjugation reactions were allowed to proceed overnight at room temperature. The conjugated Sepharose was pooled and loaded onto fritted columns, washed with 10 ml of BBS, blocked with 10 ml of 1 M glycine and washed with 10 ml 0.1 M glycine adjusted to pH 2.5 with HCl and re-neutralized in BBS. The column was washed with enough volume for the optical density at 280 nm to reach baseline.

Affinity Purification of Antibodies

The peptide affinity column was attached to a UV monitor and chart recorder. The titered rabbit antiserum was thawed and pooled. The serum was diluted with one volume of BBS and allowed to flow through the columns at 10 ml per minute. The non-peptide immunoglobulins and other proteins were washed from the column with excess BBS until the optical density at 280 nm reached baseline. The columns were disconnected and the affinity purified column was eluted using a stepwise pH gradient from pH 7.0 to 1.0. The elution was monitored at 280 nm and fractions containing antibody (pH 3.0 to 1.0) were collected directly into excess 0.5 M BBS. Excess buffer (0.5 M BBS) in the collection tubes served to neutralize the antibodies collected in the acidic fractions of the pH gradient.

The entire procedure was repeated with "depleted" serum to ensure maximal recovery of antibodies. The eluted material was concentrated using a stirred cell apparatus and a membrane with a molecular weight cutoff of 30 kD. The concentration of the final preparation was determined using an optical density reading at 280 nm. The concentration was determined using the following formula: $mg/ml=OD_{280}/1.4$.

It will be appreciated that in certain embodiments, additional steps may be used to purify antibodies of the invention. In particular, it may prove advantageous to repurify antibodies, e.g., against one of the peptides that was used in generating the antibodies. It is to be understood that the present invention encompasses antibodies that have been prepared with such additional purification or repurification steps. It will also be appreciated that the purification process may affect the binding between samples and the inventive antibodies.

Example 8

Preparing and Staining Tissue Arrays

This example describes a method that was employed to prepare the tissue arrays that were used in Examples 1-6. This example also describes how the antibody staining was performed.

Tissue arrays were prepared by inserting full-thickness cores from a large number of paraffin blocks (donor blocks) that contain fragments of tissue derived from many different patients and/or different tissues or fragments of tissues from a single patient, into a virgin paraffin block (recipient block) in a grid pattern at designated locations in a grid. A standard slide of the paraffin embedded tissue (donor block) was then made which contained a thin section of the specimen amenable to H & E staining A trained pathologist, or the equivalent versed in evaluating tumor and normal tissue, designated the region of interest for sampling on the tissue array (e.g., a tumor area as opposed to stroma). A commercially available tissue arrayer from Beecher Instruments was then used to remove a core from the donor block which was then inserted into the recipient block at a designated location. The process was repeated until all donor blocks had been inserted into the recipient block. The recipient block was then thin-sectioned to yield 50-300 slides containing cores from all cases inserted into the block.

The selected antibodies were then used to perform immunohistochemical staining using the DAKO Envision+, Peroxidase IHC kit (DAKO Corp., Carpenteria, Calif.) with DAB substrate according to the manufacturer's instructions.

Example 9

Correlating Interaction Partner Binding with Outcome/Responsiveness of Xenograft Tumors

According to the present invention, panels of useful interaction partners may be defined through analysis of human tumor cells grown in a non-human host. In particular, such analyses may define interaction partner panels whose binding correlates with prognosis and/or with responsiveness to therapy.

Cells derived from human tumors may be transplanted into a host animal (e.g., a mouse), preferably into an immunocompromised host animal. In preferred embodiments of the invention, cells (e.g., cell lines, tumor samples obtained from human patients, etc.) from a variety of different human tumors (e.g., at least 10, 20, 30, 40, 50, 60 or more different tumors) are transplanted into host animals. The animals are then treated with different (e.g., increasing) concentrations of a chemical compound known or thought to be selectively toxic to tumors with a predetermined common characteristic (e.g., class or subclass). Relative growth or regression of the tumors may then be assessed using standard techniques.

In certain embodiments of the invention, a dataset of sensitivity of the transplanted cells to a given compound or set of compounds may optionally be created. For example, a dataset might consist of the concentration of compound administered to the host animal that inhibited tumor growth 50% at 96 hr (i.e., the LD_{50}) for each of the cell samples or cell lines tested. Such a dataset, for example across at least 10, 20, 30, 40, 50, 60 or more cell lines, could then be correlated with the relative staining of the binding partners across the same cell lines. Those binding partners whose interaction (or lack thereof) with cells was highly correlated with either sensitivity to or resistance to a given compound would be useful members of a predictive panel.

Example 10

Correlating Interaction Partner Binding with Clinical Prognostic Data in Breast Cancer

According to the present invention, panels of useful interaction partners may be defined through analysis of correlations between binding patterns and clinical prognostic data. In particular, such analyses may define interaction partner panels whose binding correlates with prognosis.

The following describes the identification of exemplary panels of antibodies whose binding has been shown to correlate with the prognosis of breast cancer patients. The data was obtained using samples from the Huntsville Hospital breast cohort (the "HH breast" cohort) that was referred to in Example 3.

The HH breast cohort was generated from 1082 breast cancer patients that were treated by the Comprehensive Cancer Institute (Huntsville, Ala.) between 1990 and 2000. This larger group was filtered to a study group of 550 patients by eliminating patients according to the following criteria: 249 that had no chart which could be found; 103 that had no

clinical follow up; and 180 that did not have sufficient clinical material in the paraffin block to sample. For the remaining 550 patients, clinical data through Dec. 31, 2002 was available. Every patient in the cohort therefore had between 2 and 13 years of follow-up. The average time of follow-up among patients who did not recur was 5.6 years. Of the 550 patients, 140 had a recurrence of cancer within the study period; 353 patients were estrogen receptor positive (ER+); 154 were estrogen receptor negative (ER−); and 43 were undetermined. Some patients within these groups received adjuvant hormone therapy as shown in Table 1:

TABLE 1

	Total	Hormone	No hormone	Unknown
ER+	353	278	68	7
ER−	154	70	83	1
Undetermined	43	28	15	0

In addition, 263 patients received chemotherapy. Up to 16 different regimens were used, however, most were variants of cyclophosphamide, doxorubicin (with and without 5-fluorouracil and/or cyclophosphamide), methotrexate and 5-fluorouracil. Finally, 333 of the patients received radiation. Clinical information regarding age, stage, node status, tumor size, and grade was obtained.

The clinical information for the patients in the cohort is summarized in Table 2.

TABLE 2

	All (550)	ER+ (353)	ER− (154)
Stage = 1	236	162	49
Stage = 2	269	167	87
Stage = 3	44	23	18
Undetermined	1	0	0
Mean Age @ Dx	58	59	55
Tumor status = 0	1	0	1
Tumor status = 1	295	203	63
Tumor status = 2	195	122	62
Tumor status = 3	26	14	11
Tumor status = 4	14	6	8
Undetermined	21	8	9
Node status = 0	326	215	76
Node status = 1	205	127	71
Node status = 2	10	6	3
Undetermined	10	5	4
Metastasis = 0	527	338	147
Metastasis = 1	5	4	1
Undetermined	19	11	6

Where each category is defined in Table 3. These rules are not fixed and staging is typically done by an oncologist based on TNM status and other factors. These definitions for staging will not necessarily match with the stage that each patient was actually given. Node status is the primary tool for staging purposes.

TABLE 3

Tumor status = 0	No evidence of tumor				
Tumor status = 1	<2 cm				
Tumor status = 2	2-5 cm				
Tumor status = 3	>5 cm				
Tumor status = 4	Any size but extends to chest wall				
Node status = 0	No regional LN metastasis				
Node status = 1	Ancillary LN metastasis but nodes still moveable				
Node status = 2	Ancillary LN metastasis with nodes fixed to each other OR internal mammary node metastasis				
Metastasis = 0	No distant metastasis				
Metastasis = 1	Distant metastasis				
Stage = 1	T1, N0, M0				
Stage = 2	T0, N1, M0	T1, N1, M0	T2, N0, M0	T2, N1, M0	T3, N0, M0
Stage = 3	T(0-3), N2, M0	T3, N1, M0	T4, NX, M0		
Stage = 4	TX, NX, M1				

Samples from patients in the cohort were stained with antibodies from the breast cancer classification panel identified in Appendix A (as previously described in Examples 2 and 3). The stained samples were then scored in a semi-quantitative fashion, with 0=negative, 1=weak staining, and 2=strong staining When appropriate, alternative scoring systems were used (i.e., 0=negative, 1=weak or strong; or 0=negative or weak and 1=strong staining) For each antibody, the scoring system used was selected to produce the most significant prognostication of the patients, as determined by a log-rank test (e.g., see Mantel and Haenszel, *Journal of the National Cancer Institute* 22:719-748, 1959). The results are presented in Appendix C and are grouped into four categories that have been clinically recognized to be of significance: all patients, ER+ patients, ER− patients, and ER+/node− patients. As shown, the antibodies were found to have differing significances for each of these categories of breast cancer patients.

It is to be understood that exclusion of a particular antibody from any prognostic panel based on these experiments is not determinative. Indeed, it is anticipated that additional data with other samples may lead to the identification of other antibodies (from Appendix A and beyond) that may have prognostic value for these and other classes of patients.

The expected relationship between the staining of patient samples with each antibody and the recurrence of tumors was measured using the Kaplan-Meier estimate of expected recurrence (e.g., see Kaplan and Meier, *J. Am. Stat. Assn.* 53:457-81, 1958). The log-rank test was used to determine the significance of different expected recurrences for each antibody (e.g., see Mantel and Haenszel, *Journal of the National Cancer Institute,* 22:719-748, 1959). This produces the p-value that is listed for each antibody in Appendix C. Preferred antibodies are those that produce a p-value of less than 0.10.

The degree to which these antibodies predicted recurrence was determined using a Cox univariate proportional hazard model (e.g., see Cox and Oakes, "Analysis of Survival Data", Chapman & Hall, 1984). The "hazard ratio" listed in Appendix C for each antibody reflects the predicted increase in risk of recurrence for each increase in the staining score. Scores greater than 1.0 indicate that staining predicts an increased risk of recurrence compared to an average individual, scores less than 1.0 indicate that staining predicts a decreased risk.

It will be appreciated that these antibodies can be used alone or in combinations to predict recurrence (e.g., in combinations of 2, 3, 4, 5, 6, 7, 8, 9, 10 or more antibodies). It will also be appreciated that while a given antibody may not predict recurrence when used alone the same antibody may predict recurrence when used in combination with others. It will also be understood that while a given antibody or combination of antibodies may not predict recurrence in a given set of patients (e.g., ER+ patients), the same antibody or combination of antibodies may predict recurrence in a different set of patients (e.g., ER− patients). Similarly, it is to be understood that while a given antibody or combination of antibodies may not predict recurrence in a given set of patients (e.g., ER+ patients), the same antibody or combination of antibodies may predict recurrence in a subset of these patients (e.g., ER+/node negative patients).

These prognostic panels could be constructed using any method. Without limitation these include simple empirically derived rules, Cox multivariate proportional hazard models (e.g., see Cox and Oakes, "Analysis of Survival Data", Chapman & Hall, 1984), regression trees (e.g., see Segal and Bloch, *Stat. Med.* 8:539-50, 1989), and/or neural networks (e.g., see Ravdin et al., *Breast Cancer Res. Treat.* 21:47-53, 1992). In certain embodiments a prognostic panel might include between 2-10 antibodies, for example 3-9 or 5-7 antibodies. It will be appreciated that these ranges are exemplary and non-limiting.

The prognostic value of exemplary panels of antibodies were also assessed by generating Kaplan-Meier recurrence curves for ER+ and ER+/node− patients and then comparing these with curves produced for these same patients with the standard Nottingham Prognostic Index (NPI).

In order to generate Kaplan-Meier curves based on antibody panels, Cox univariate proportional hazard regression models were first run with all antibodies from Appendix C utilizing all three scoring procedures. The antibodies and scoring systems best able to predict recurrence were then used in a regression tree model and pruned to maintain predictive power while reducing complexity. Patients whom the panel predicted as being strongly likely to recur were placed in the "poor" prognosis group. Patients whom the panel predicted as being strongly unlikely to recur were given the prediction of "good". Patients whom the panel predicted as neither being strongly likely to recur or not recur were placed in the "moderate" prognosis group. Kaplan-Meier curves were then calculated based on recurrence data for patients within each group. FIG. **4**A show the curves that were obtained for ER+ patients in each of these prognostic groups. FIG. **5**A show the curves that were obtained for ER+/node− patients in each of these prognostic groups.

The antibodies from Appendix C that were used to predict recurrence for ER+ patients (FIG. **4**A) were: s0296P1 (1:225 dilution, scoring method 3), s6006 (1:1 dilution, scoring method 2), s0545 (1:900 dilution, scoring method 2), s0063 (1:300 dilution, scoring method 2), s6002 (1:1 dilution, scoring method 3), s0081 (1:20 dilution, scoring method 2), s0255 (1:1000 dilution, scoring method 3), and s0039 (1:100 dilution, scoring method 2).

The antibodies from Appendix C that were used to predict recurrence for ER+/node− patients (FIG. **5**A) were: s0143P3 (1:630 dilution, scoring method 1), s0137 (1:2500 dilution, scoring method 2), s0260 (1:5400 dilution, scoring method 2), s0702 (1:178200 dilution, scoring method 2), s0545 (1:900 dilution, scoring method 2), s6002 (1:1 dilution, scoring method 1), s6007 (1:1 dilution, scoring method 1).

Kaplan-Meier recurrence curves were then generated for the same patients based on their standard NPI scores. NPI scores were calculated for patients according to the standard formula NPI=(0.2×tumor diameter in cm)+lymph node stage+tumor grade. As is well known in the art, lymph node stage is either 1 (if there are no nodes affected), 2 (if 1-3 glands are affected) or 3 (if more than 3 glands are affected). The tumor grade was scored according to the Bloom-Richardson Grade system (Bloom and Richardson, *Br. J. Cancer* 11:359-377, 1957). According to this system, tumors were examined histologically and given a score for the frequency of cell mitosis (rate of cell division), tubule formation (percentage of cancer composed of tubular structures), and nuclear pleomorphism (change in cell size and uniformity). Each of these features was assigned a score ranging from 1 to 3 as shown in Table 4. The scores for each feature were then added together for a final sum that ranged between 3 to 9. A tumor with a final sum of 3, 4, or 5 was considered a Grade 1 tumor (less aggressive appearance); a sum of 6 or 7 a Grade 2 tumor (intermediate appearance); and a sum of 8 or 9 a Grade 3 tumor (more aggressive appearance).

TABLE 4

	Score
Tubule formation (% of carcinoma composed of tubular structures)	
>75%	1
10-75%	2
<10%	3
Nuclear pleomorphism (Change in Cells)	
Small, uniform cells	1
Moderate increase in size and variation	2
Marked variation	3
Mitosis Count (Cell Division)	
Up to 7	1
8 to 14	2
15 or more	3

Patients with tumors having an overall NPI score of less than 3.4 were placed in the "good" prognosis group. Those with an NPI score of between 3.4 and 5.4 were placed in the "moderate" prognosis group and patients with an NPI score of more than 5.4 were placed in the "poor" prognosis group. Kaplan-Meier curves were then calculated based on recurrence data for patients within each group. FIG. **4**B show the curves that were obtained for ER+ patients in each of these NPI prognostic groups. FIG. **5**B show the curves that were obtained for ER+/node− patients in each of these NPI prognostic groups. By definition ER+/node− patients have an NPI score that is less than 5.4. This explains why there is no "poor" prognosis curve in FIG. **5**B. Example 12 describes other exemplary prognostic panels for breast cancer patients.

Example 11

Correlating Interaction Partner Binding with Clinical Prognostic Data in Lung Cancer

This Example describes the identification of exemplary panels of antibodies whose binding has been shown to correlate with the prognosis of lung cancer patients. The data was obtained using samples from the Huntsville Hospital lung cohort (the "HH lung" cohort) that was referred to in Example 5.

The HH lung cohort was generated from 544 lung cancer patients that were treated by the Comprehensive Cancer Institute (Huntsville, Ala.) between 1987 and 2002. This larger group was filtered to a study group of 379 patients by eliminating patients that had insufficient clinical follow up or that did not have sufficient clinical material in the paraffin block to sample. For the remaining patients, clinical data through Sep. 30, 2003 was available. This set of patients consisted of 232 males and 147 females. The average time of follow-up among patients who did not recur was 3.5 years. Of the 379 patients, 103 had a recurrence of cancer within the study period. All patients in this study were diagnosed at a pathological stage of 1 or 2, with 305 patients at stage 1, 1A, or 1B, and 74 patients at stage 2, 2A, or 2B.

Samples from patients in the cohort were stained with antibodies from the lung cancer classification panel identified in Appendix A (as previously described in Examples 4 and 5). The stained samples were then scored in a semi-quantitative fashion; scoring methods 1-3 use the following schemes: method 1 (0=negative; 1=weak; 2=strong); method 2 (0=negative; 1=weak or strong); and method 3 (0=negative or weak; 1=strong). For each antibody, the scoring system used was selected to produce the most significant prognostication of the patients, as determined by a log-rank test (e.g., see Mantel and Haenszel, *Journal of the National Cancer Institute* 22:719-748, 1959). The results are presented in Appendix D and are grouped into three categories that have been clinically recognized to be of significance: all patients, adenocarcinoma patients, and squamous cell carcinoma patients. As shown, the antibodies were found to have differing significances for each of these categories of lung cancer patients.

It is to be understood that exclusion of a particular antibody from any prognostic panel based on these experiments is not determinative. Indeed, it is anticipated that additional data with other samples may lead to the identification of other antibodies (from Appendix A and beyond) that may have prognostic value for these and other classes of patients.

As for the breast study of Example 10, the expected relationship between the staining of patient samples with each antibody and the recurrence of tumors was measured using the Kaplan-Meier estimate of expected recurrence and a log-rank test was used to determine the significance of different expected recurrences. This produces the p-value that is listed for each antibody in Appendix D. Preferred antibodies are those that produce a p-value of less than 0.10.

The degree to which these antibodies predicted recurrence was determined using a Cox univariate proportional hazard model. The "hazard ratio" listed in Appendix D for each antibody reflects the predicted increase in risk of recurrence for each increase in the staining score. Scores greater than 1.0 indicate that staining predicts an increased risk of recurrence compared to an average individual, scores less than 1.0 indicate that staining predicts a decreased risk.

As a number of patients had information regarding whether or not the cancer recurred but lacked information on time to recurrence, a chi-square test was also performed. This standard statistical test shows the degree of divergence between observed and expected frequencies and does not employ time to recurrence, as does the log-rank test. Preferred antibodies are those that produce a p-value of less than 0.10.

It will be appreciated that these prognostic antibodies can be used alone or in combinations to predict recurrence (e.g., in combinations of 2, 3, 4, 5, 6, 7, 8, 9, 10 or more antibodies). It will also be appreciated that while a given antibody may not predict recurrence when used alone, the same antibody may predict recurrence when used in combination with others. It will also be understood that while a given antibody or combination of antibodies may not predict recurrence in a given set of patients (e.g., adenocarcinoma patients), the same antibody or combination of antibodies may predict recurrence in a different set of patients (e.g., squamous cell carcinoma patients).

As for the breast study of Example 10, these prognostic panels could be constructed using any method. Without limitation these include simple empirically derived rules, Cox multivariate proportional hazard models, regression trees, and/or neural networks. In certain embodiments a prognostic panel might include between 2-10 antibodies, for example 3-9 or 5-7 antibodies. It will be appreciated that these ranges are exemplary and non-limiting. The construction of exemplary prognostic panels for lung cancer patients is described in Example 13.

Example 12

Prognostic Breast Cancer Panels

This Example builds on the results of Example 10 and describes the identification of additional exemplary panels of antibodies whose binding has been shown to correlate with the prognosis of breast cancer patients.

First, the individual prognostic ability of the antibodies of Appendix C was refined using samples from the HH breast cohort that was described in Example 2. In particular, certain antibodies were excluded based on subjective assessment of specificity and scoreability. The methodology paralleled that used in Example 10 and the updated antibody data is presented in Appendix E.

Second, prognostic panels in two currently identified clinically important subclasses of breast cancer patients were generated, namely ER+/node− patients and ER− patients. To minimize the chance of identifying spurious associations, only those antibodies from Appendix E that showed sufficient significance (p-value of less than 0.10) in either the ER+ or ER+/node− patient classes were used in creating prognostic panels for the ER+/node− patients, and only the similarly significant markers from the ER− patient set for creating a prognostic panel for the ER− patients. Using Cox proportional hazard analysis and regression tree analysis (as described in Example 10) candidate panels (and dendrograms for regression tree analysis) were derived for prediction of early recurrence. For both ER+/node− patients and ER− patients, panels and dendrograms were chosen that identified patients with significantly increased risks of recurrence.

Prognostic Panels Generated by Cox Analysis

Cox proportional hazard analysis treats the component antibodies of a panel as additive risk factors. The panels for the specified patient classes were created by initially using all applicable antibodies, and then iteratively removing antibodies from the panel. If the removal of an antibody increased or did not affect the significance and prognostic ability of the panel as a whole, it was excluded, otherwise it was retained. In this manner preferred panels with minimal numbers of antibodies were created. The preferred panels for ER+/node− and ER− patients are presented in Tables 5 and 6, respectively. Antibodies within the preferred panels are ranked based on their relative contributions to the overall prediction function.

TABLE 5

Panel	Analysis	P value[1]	Hazard ratio[2]
Breast ER+/node-	Cox	8.17E−05	5.68
AGI ID	Rank	P value[3]	Terms[4]
S0702/s0296P1	1	0.00015	−0.213, 1.330
s6006	2	0.00660	−0.325, 0.799
s0404	3	0.06200	−0.099, 0.958
s0545	4	0.10000	−0.112, 0.604
s0235	5	0.25000	−0.114, 0.390

[1]P value of overall panel

[2]Hazard ratio of overall panel

[3]P value of the contribution of a given antibody to the overall panel

[4]Contribution of given antibody to overall panel prediction function depending on IHC score (e.g., scores of 0 or 1 for s6006 which uses scoring method 2 [see Appendix E] result in its term in the model equaling −0.325 or 0.799, respectively).

TABLE 6

Panel	Analysis	P value[1]	Hazard ratio[2]
Breast ER−	Cox	3.10E−03	2.25
AGI ID	Rank	P value[3]	Terms[4]
s0691	1	0.04700	−0.163, 0.436, 0.640
s0545	2	0.08900	−0.339, 0.259
s0330x1	3	0.57000	0.510, −5.560

[1,2,3,4]See Table 5

The prognostic value of these exemplary panels were assessed by generating Kaplan-Meier recurrence curves for ER+/node− and ER− patients. Patients whom the panels predicted as being strongly likely to recur were placed in the "bad" prognosis group. Patients whom the panels predicted as being strongly unlikely to recur were given the prediction of "good". Patients whom the panels predicted as neither being strongly likely to recur or not recur were placed in the "moderate" prognosis group. Kaplan-Meier curves were then calculated based on recurrence data for patients within each group. FIG. **6** shows the curves that were obtained for ER+/node− patients in each of these prognostic groups. FIG. **7** shows the curves that were obtained for ER− patients in each of these prognostic groups.

When lymph node status was included as an additional variable for the ER− patient set the preferred panel was as shown in Table 7.

TABLE 7

Panel	Type	P value[1]	Hazard ratio[2]
Breast ER−	Cox plus node	3.70E−05	3.93
AGI ID	Rank	P value[3]	Terms[4]
s6007	1	0.05000	−0.460, 0.280
s0545	2	0.06400	−0.400, 0.290
s0068	3	0.18000	−0.350, 0.160
s0330x1	4	0.62000	−5.820, 0.450

[1,2,3,4]See Table 5

The prognostic value of this exemplary panel was also assessed by generating Kaplan-Meier recurrence curves for ER− patients. Patients whom the panel predicted as being strongly likely to recur were placed in the "bad" prognosis group. Patients whom the model predicted as being strongly unlikely to recur were given the prediction of "good". Patients whom the model predicted as neither being strongly likely to recur or not recur were placed in the "moderate" prognosis group. Kaplan-Meier curves were then calculated based on recurrence data for patients within each group. FIG. **8** shows the curves that were obtained for ER− patients in each of these prognostic groups.

While the preferred Cox panels of the invention for ER+/node− and ER− patients include each of the listed antibodies, it is to be understood that other related panels are encompassed by the present invention. In particular, it will be appreciated that the present invention is in no way limited to the specific antibodies listed. For example, other antibodies directed to the same biomarker(s) may be used (e.g., taking the Cox ER+/node− panel, it can be readily seen from Appendix A that antibodies s0702 or s0296P1 can be replaced with other antibodies directed to biomarker Hs.184601; antibody s6006 can be replaced with other antibodies directed to biomarker Hs.1846, etc.). As noted, addition of certain antibodies from Appendix E had no effect on the significance and prognostic ability of the panel as a whole. Thus, antibodies may be added to any given panel without necessarily diminishing the utility of a panel for patient prognosis. The inclusion of antibodies beyond those listed in Appendix E is also within the scope of the invention. In certain embodiments less than all of the listed antibodies may be used in a prognostic panel.

Generally, a Cox panel for ER+/node− patients will include at least two antibodies selected from the group consisting of antibodies directed to biomarkers Hs.184601, Hs.1846, Hs.75789, Hs.63609 and Hs.220529 (e.g., s0702 and/or s0296P1, s6006, s0404, s0545 and s0235, see Table 5 and Appendix A). Preferably, the panel will include an antibody directed to biomarker Hs.184601 and at least one antibody directed to a biomarker selected from the group consisting of Hs.1846, Hs.75789, Hs.63609 and Hs.220529. All permutations of these antibodies are encompassed. In one embodiment an antibody to biomarker Hs.184601 (e.g., s0702 and/or s0296P1) is used with an antibody to biomarker Hs.1846 (e.g., s6006). In another embodiment an antibody to biomarker Hs.184601 is used with antibodies to biomarkers Hs.1846 and Hs.75789 (e.g., s6006 and s0404). In other embodiments an antibody to biomarker Hs.184601 is used with antibodies to biomarkers Hs.1846, Hs.75789, Hs.63609 and optionally Hs.220529 (e.g., s6006, s0404, s0545 and optionally s0235). In preferred embodiments an antibody to Hs.184601 is used with antibodies to biomarkers Hs.1846, Hs.75789, Hs.63609 and Hs.220529.

Similarly, a Cox panel for ER− patients will include at least two antibodies selected from the group consisting of antibodies directed to biomarkers Hs.6682, Hs.63609 and Hs.306098 (e.g., s0691, s0545 and s0330×1, see Table 6 and Appendix A). Preferably, the panel will include an antibody directed to biomarker Hs.6682 and antibodies to one or both of biomarkers Hs.63609 and Hs.306098. In preferred embodiments an antibody to biomarker Hs.6682 is used with antibodies to biomarkers Hs.63609 and Hs.306098.

When lymph node status is used as an additional variable, an inventive prognostic Cox panel for ER− patients will include at least two antibodies selected from the group consisting of antibodies directed to biomarkers Hs.80976, Hs.63609, Hs.416854 and Hs.306098 (e.g., s6007, s0545, s0068 and s0330×1, see Table 7 and Appendix A). Preferably, the panel will include an antibody directed to biomarker Hs.80976 and antibodies to one or more of biomarkers Hs.63609, Hs.416854 and Hs.306098. All permutations of these antibodies are encompassed. In one embodiment an antibody to biomarker Hs.80976 is used with an antibody to biomarker Hs.63609. In another embodiment an antibody to biomarker Hs.80976 is used with antibodies to biomarkers Hs.63609 and Hs.416854 and optionally with a biomarker to

Hs.306098. In preferred embodiments an antibody to biomarker Hs.80976 is used with antibodies to biomarkers Hs.63609, Hs.416854 and Hs.306098.

The present invention also encompasses methods of assessing the prognosis of a patient having a breast tumor using these exemplary panels. After obtaining a tumor sample from a patient with unknown prognosis the sample is contacted with two or more antibodies from the panels of Tables 5, 6 and/or 7. The patient's likely prognosis is then assessed based upon the pattern of positive and negative binding of the two or more antibodies to the tumor sample.

Prognostic Panels Generated by Regression Tree Analysis

Regression trees classify the patients into a number of subclasses each defined by their pattern of binding to a unique set of antibodies from within a panel. An exemplary tree (or "dendrogram") for ER+/node− patients is shown in FIG. **9** which is discussed below. Regression trees were initially created with all applicable antibodies, and then "pruned" to a minimal complexity (least number of terminal nodes without losing too much prognostic ability) using a cross validation procedure. This cross validation procedure involved building panels and dendrograms using a series of patient groups that were picked from the total patient set using a series of increasingly pruned trees. The results over the tested groups were summed and the minimally complex least error-prone panel and dendrogram were chosen. The resulting dendrogram was further simplified by placing nodes with a range of response values into the classes "good" or "poor" (or alternatively "good", "moderate" or "poor"). Table 8 lists the antibodies of an exemplary ER+/node− tree panel that was constructed as described above. The dendrograms for this panel is illustrated in FIG. **9**.

TABLE 8

Panel	Analysis	P value[1]	Hazard ratio[2]
Breast ER+/node-	Tree	2.82E−05	6.06
AGI ID		Rank	
s0702/s0296P1		1	
s0081		2	
s6006		2	
s6007		3	
s0545		4	
s6002		4	

[1]P value of overall panel
[2]Hazard ratio of overall panel

As illustrated in FIG. **9**, if a patient is positive for staining at a given node his or her prognosis decision tree follows the branch marked with a "+". Conversely if a patient is negative for staining at a given node his or her prognosis decision tree follows the branch marked "−". This is done until a terminus is reached.

For example, if patient A is positive for staining with s0702 and negative for staining with s0081 then, based on the dendrogram, his or her prognosis is "bad". In contrast, if patient B is negative for staining with s0702, negative for staining with s6006, positive for staining with s6007 and negative for staining with s0545 then his or her prognosis is "good". It will be appreciated from the foregoing and FIG. **9** that the number of stains required in order to yield a prognosis will vary from patient to patient. However, from a practical standpoint (and without limitation), it may prove advantageous to complete all the stains for a given panel in one sitting rather than adopting an iterative approach with each individual antibody.

The prognostic value of the exemplary panel of Table 8 was also assessed by generating Kaplan-Meier recurrence curves for ER+/node− patients. Patients whom the panel predicted as being strongly likely to recur were placed in the "bad" prognosis group. Patients whom the panel predicted as being strongly unlikely to recur were given the prediction of "good". Patients whom the panel predicted as neither being strongly likely to recur or not recur were placed in the "moderate" prognosis group. Kaplan-Meier curves were then calculated based on recurrence data for patients within each group. FIG. **10** shows the curves that were obtained for ER+/node− patients in each of these prognostic groups.

Generally, a tree panel for ER+/node− patients will include an antibody to biomarker Hs.184601 (e.g., s0702 or s0296P1) with antibodies to one or both of biomarkers Hs.155956 and Hs.1846 (e.g., s0081 and s6006, see Table 8 and Appendix A). In certain embodiments an antibody to biomarker Hs.80976 (e.g., s6007) may be added, optionally with antibodies to one or both of biomarkers Hs.63609 and Hs.2905 (e.g., s0545 and s6002). In preferred embodiments, the tree panel includes an antibody to biomarker Hs.184601 and antibodies to biomarkers Hs.155956, Hs.1846, Hs.80976, Hs.63609 and Hs.2905.

Table 9 lists the antibodies of exemplary ER+ and ER− tree panels that were constructed as described above for the ER+/node− tree panel of Table 8. The dendrograms for theses panels are illustrated in FIG. **11**.

TABLE 9

Panel	Analysis	Panel	Analysis
Breast ER+	Tree	Breast ER−	Tree
AGI ID	Rank	AGI ID	Rank
s0702/s0296P1	1	s6007	1
s0137	2	s0303	2
s6007	2	s0398	2
s5076	3	s0063	3
s0143	3	s0545	4
s6007	4	s0702/s0296P1	4
s0545	4	s0068	5

The present invention also encompasses methods of assessing the prognosis of a patient having a breast tumor using an inventive tree panel. For example, after obtaining a tumor sample from a patient with unknown prognosis the sample is contacted with two or more antibodies from the panel of Table 8 (or one of the panels in Table 9). The patient's likely prognosis is then assessed based upon the positive or negative binding of the two or more antibodies to the tumor sample using the dendrogram of FIG. **9** (or FIG. **11**). Taking the ER+/node− panel of Table 8 as an example, the method generally includes a step of contacting the tumor sample with an antibody to biomarker Hs.184601 (e.g., s0702 or s0296P1) and antibodies to one or both of biomarkers Hs.155956 and Hs.1846 (e.g., s0081 and/or s6006). In other embodiments the tumor sample is further contacted with an antibody to biomarker Hs.80976 (e.g., s6007) and optionally with antibodies to biomarkers Hs.63609 and/or Hs.2905 (e.g., s0545 and/or s6002). As mentioned above, the tumor sample may be contacted with these antibodies in a single sitting or sequentially based on the binding results of a previous stain. Obviously the tumor sample may be divided and different antibodies contacted with different fractions. Alternatively different original tumor samples may be contacted with different antibodies.

Whether created by Cox or regression tree analysis, the exemplary prognostic panels were determined to be independent of age, stage, and grade. To ensure that the panels were

not identifying classes of patients unlikely to be found to be significant in an independent cohort, cross validation was used to estimate the error inherent in each panel. Ten-fold cross-validation was performed by sequentially "leaving-out" 10% of patients and building panels on the remaining patients ten times such that all patients were ultimately classified. This included re-determining the set of antibodies sufficiently significant to be employed in the panel building process (p-value <0.10). Cross validated p-values reflect the confidence calculated for the sum of the ten independent panels and confirmed the statistical significance of these panels. For the ER+/node– patient set, both the Cox (Table 5) and regression tree (Table 8) panels showed significance after cross-validation (p-value/hazard ratio of 1.12E-02/2.36 and 3.40E-03/2.91, respectively). For the ER– patient set, the Cox panels (Tables 6-7) were also shown to be able to retain significance (p-value/hazard ratios of 6.40E-02/1.37 and 1.80E-03/1.79 for the panels of Table 6 and 7, respectively).

It is to be understood that each of the exemplary Cox and tree panels described herein may be used alone, in combination with one another (e.g., the Cox panel of Table 5 and the tree panel of Table 8 for ER+/node– patients) or in conjunction with other panels and/or independent prognostic factors.

Example 13

Prognostic Lung Cancer Panels

This Example builds on the results of Example 11 and describes the identification of exemplary panels of antibodies whose binding has been shown to correlate with the prognosis of lung cancer patients.

Prognostic panels in two currently identified clinically important subclasses of lung cancer patients were generated, namely adenocarcinoma and squamous cell carcinoma patients. Consistent with the known clinical significance of diagnoses of these two subclasses of lung cancer patients it was found that the most robust models were derived when patients were first classified in this manner, and then the separate patient groups modeled independently. It will be appreciated that this approach is non-limiting and that models could be generated using all lung cancer patients or using other subclasses of patients. To minimize the chance of identifying spurious associations, only those antibodies from Appendix D that showed sufficient significance (p-value of less than 0.10) in the adenocarcinoma patient class were used in creating prognostic panels for the adenocarcinoma patients, and only the similarly significant markers from the squamous cell carcinoma patient class for creating a prognostic panel for the squamous cell carcinoma patients. Using Cox proportional hazard analysis (as described in Example 10) candidate panels were derived for prediction of early recurrence. For both adenocarcinoma and squamous cell carcinoma patients, panels were chosen that identified patients with significantly increased risks of recurrence.

As previously noted, Cox proportional hazard analysis treats the component antibodies of a panel as additive risk factors. The panels for the specified patient classes were created by initially using all applicable antibodies, and then iteratively removing antibodies from the panel. If the removal of an antibody increased or did not affect the significance and prognostic ability of the panel as a whole, it was excluded, otherwise it was retained. In this manner preferred panels with minimal numbers of antibodies were created. The preferred panels for squamous cell carcinoma and adenocarcinoma patients are presented in Tables 10 and 11, respectively. Antibodies within the preferred panels are ranked based on their relative contributions to the overall prediction function.

TABLE 10

Panel	Analysis	P value[1]	Hazard ratio[2]
Lung squamous	Cox	3.20E–05	6.88
AGI ID	**Rank**	**P value[3]**	**Terms[4]**
s0022	1	0.00620	0.880, –1.240
s0702/s0296P1	2	0.12000	0.980, –0.150
s0330	3	0.13000	0.870, –0.034
s0586	4	0.16000	0.680, –0.250

[1]P value of overall panel
[2]Hazard ratio of overall panel
[3]P value of the contribution of a given antibody to the overall panel
[4]Contribution of given antibody to overall panel prediction function depending on IHC score (e.g., scores of 0 or 1 for s0022 which uses scoring method 2 [see Appendix D] result in its term in the model equaling 0.880 or –1.240, respectively).

TABLE 11

Panel	Analysis	P value[1]	Hazard ratio[2]
Lung adenocarcinoma	Cox	1.30E–05	3.23
AGI ID	**Rank**	**P value[3]**	**Terms[4]**
s6013	1	0.02000	–0.430, 0.520
s0545	2	0.03500	–0.070, 1.150
s0404	3	0.04000	–0.270, 0.550
s0702/s0296P1	4	0.08800	–0.230, 0.450

[1,2,3,4]See Table 10

The prognostic value of these exemplary panels were assessed by generating Kaplan-Meier recurrence curves for the combined lung cancer patients of the HH lung cohort. Patients were initially classified as adenocarcinoma or squamous cell carcinoma patients. For each patient the pattern of antibody staining with the applicable panel (i.e., Table 10 or 11) was then assessed. Patients whom the panels predicted as being strongly likely to recur were placed in the "bad" prognosis group. Patients whom the panels predicted as being strongly unlikely to recur were given the prediction of "good". Patients whom the panels predicted as neither being strongly likely to recur or not recur were placed in the "moderate" prognosis group. Kaplan-Meier curves were then calculated based on five year recurrence data for patients within each group. FIG. **12** shows the curves that were obtained when the combined lung cancer patients were placed in "good", "moderate" or "bad" prognosis groups. FIG. **13** shows the curves that were obtained when patients in the "moderate" and "bad" groups were combined into a single "bad" prognostic group.

To ensure that the panels were not identifying classes of patients unlikely to be found to be significant in an independent cohort, cross validation was used to estimate the error inherent in each panel. Ten-fold cross-validation was performed by sequentially "leaving-out" 10% of patients and building panels on the remaining patients ten times such that all patients were ultimately classified. This included re-determining the set of antibodies sufficiently significant to be employed in the panel building process (p-value <0.10). Cross validated p-values reflect the confidence calculated for the sum of the ten independent panels and confirmed the statistical significance of these panels. The panels showed significance after cross-validation with the combined lung patients (p-value/hazard ratio of 2.20E-02/1.48 when a

"good", "moderate" and "bad" scheme was used and 1.80E-02/2.07 when a "good" and "bad" scheme was used).

While preferred Cox panels of the invention for lung cancer patients include each of the listed antibodies, it is to be understood that other related panels are encompassed by the present invention. In particular, it will be appreciated that the present invention is in no way limited to the specific antibodies listed. For example, other antibodies directed to the same biomarker(s) may be used (e.g., taking the squamous cell carcinoma panel, it can be readily seen from Appendix A that antibody s0022 can be replaced with other antibodies directed to biomarker Hs.176588; s0702 or s0296P1 can be replaced with other antibodies directed to biomarker Hs.184601, etc.). Other antibodies from Appendix D may be added to any given panel without necessarily diminishing the utility of a panel for patient prognosis. The inclusion of antibodies beyond those listed in Appendix D is also within the scope of the invention. In certain embodiments less than all of the listed antibodies may be used in a prognostic panel.

Generally, a Cox panel for squamous cell carcinoma patients will include at least two antibodies selected from the group consisting of antibodies directed to biomarkers Hs.176588, Hs.184601, Hs.306098 and Hs.194720 (e.g., s0022, s0702 or s0296P1, s0330 and s0586, see Table 10 and Appendix A). Preferably, the panel will include an antibody directed to biomarker Hs.176588 and at least one antibody directed to a biomarker selected from the group consisting of Hs.184601, Hs.306098 and Hs.194720. All permutations of these antibodies are encompassed. In one embodiment an antibody to biomarker Hs.176588 (e.g., s0022) is used with an antibody to biomarker Hs.184601 (e.g., s0702 and/or s0296P1). In another embodiment an antibody to biomarker Hs.176588 is used with antibodies to biomarkers Hs.184601 and Hs.306098 (e.g., s0702 or s0296P1 and s0330). In preferred embodiments an antibody to biomarker Hs.176588 is used with antibodies to biomarkers Hs.184601, Hs.306098 and Hs.194720.

Similarly, a Cox panel for adenocarcinoma patients will include at least two antibodies selected from the group consisting of antibodies directed to biomarkers Hs.323910, Hs.63609, Hs.75789 and Hs.184601 (e.g., s6013, s0545, s0404 and s0702 or s0296P1, see Table 11 and Appendix A). Preferably, the panel will include an antibody directed to biomarker Hs.323910 and at least one antibody directed to a biomarker selected from the group consisting of Hs.63609, Hs.75789 and Hs.184601. All permutations of these antibodies are encompassed. In one embodiment an antibody to biomarker Hs.323910 (e.g., s6013) is used with an antibody to biomarker Hs.63609 (e.g., s0545). In another embodiment an antibody to biomarker Hs.323910 is used with antibodies to biomarkers Hs.63609 and Hs.75789 (e.g., s0545 and s0404). In preferred embodiments an antibody to biomarker Hs.323910 is used with antibodies to biomarkers Hs.63609, Hs.75789 and Hs.184601.

It is to be understood that these exemplary Cox panels may be used alone, in combination with one another or in conjunction with other panels and/or independent prognostic factors.

The present invention also encompasses methods of assessing the prognosis of a patient having a lung tumor using these exemplary panels. After obtaining a tumor sample from a patient with unknown prognosis the sample is contacted with two or more antibodies from the panels of Table 10 and/or 11. The patient's likely prognosis is then assessed based upon the positive or negative binding of the two or more antibodies to the tumor sample.

Example 14

Use of Prognostic Lung Cancer Panels with an Independent Cohort

This Example builds on the results of Example 13 by describing how the exemplary prognostic lung cancer panels were used to predict recurrence in an independent cohort of lung cancer patients.

A cohort of 119 lung cancer patients from the University of Alabama-Birmingham (UAB) was used for this purpose. Relatively limited clinical data was available for these patients, in most cases only survival time was available. The average time of follow-up among patients who did not die of disease was 28 months. Of the 119 patients, 54 were noted to have had a recurrence of cancer within the study period, and 74 died of disease. This cohort differed significantly from the HH lung cohort (see Example 11) in that it was not limited to early stage tumors, and therefore the cohort had a greater incidence of death due to disease. Since recurrence data for this cohort was limited, the prognostic panels of Example 13 (designed to predict recurrence) were used to predict survival in this independent cohort. Specifically, the prognostic value of the panels were assessed by generating Kaplan-Meier survival curves for the combined lung cancer patients of the UAB cohort. As in Example 13, patients were initially classified as adenocarcinoma or squamous cell carcinoma patients. For each patient the pattern of antibody staining with the applicable panel (i.e., Table 10 or 11) was then assessed. Patients were placed in "bad", "moderate" and "good" prognosis groups based on their binding patterns with these antibodies. Kaplan-Meier curves were then calculated based on survival data for patients within each group. FIG. **14** shows the curves that were obtained when the combined lung cancer patients were placed in "good", "moderate" or "bad" prognosis groups (p-value/hazard ratio of 5.20E-02/1.98). FIG. **15** shows the curves that were obtained when the patients in the "moderate" and "bad" groups were combined into a single "bad" prognostic group (p-value/hazard ratio of 2.50E-02/3.03). FIG. **16** shows the curves that were obtained when the subclass of adenocarcinoma patients were placed in "good", "moderate" or "bad" prognosis groups (no patients fell within the "bad" group hence there are only two curves, p-value/hazard ratio of 4.00E-02/2.19). FIG. **17** shows the curves that were obtained when the subclass of squamous cell carcinoma patients were placed in "good", "moderate" or "bad" prognosis groups (p-value/hazard ratio of 2.50E-02/3.03).

The prognostic significance of individual antibodies identified in the HH lung cohort (i.e., those listed in Appendix D) were also reassessed using the five year survival data from the UAB cohort. The methodology was as described in Example 11. The prognostic significance of these same antibodies was also recalculated using five year recurrence data from the HH lung cohort (instead of the complete follow-up period as in Example 11 where patients who did not die of disease were followed for a period of up to ten years). Based on these calculations, several antibodies from Appendix D were found to have a relatively significant individual prognostic value (p-value less than 0.2) in both the HH and UAB lung cohorts. These antibodies are presented in Appendix F.

Example 15

Use of a Lung Cancer Classification Panel with an Independent Cohort

The pattern of reactivity with the lung cancer classification panel of Example 5 (see Appendix A) was determined using samples from the HH lung cohort (data not shown). As in Example 4, patients were classified using k-means clustering. Seven sub-classes of lung cancer patients were chosen by their consensus pattern of staining.

The morphology of the lung cancers within each sub-class were determined and are shown graphically in FIG. **18**. Interestingly, the sub-classes were found to comprise patients with lung cancers having similar morphological characteristics (i.e., sub-classes 1, 2, 3 and 7 were composed of a majority of patients with adenocarcinomas; sub-classes 4 and 5 were composed of a majority of patients with squamous cell carcinomas and sub-class 6 was composed of a majority of patients with large cell carcinomas). These results suggest that the antibodies in the classification panel are recognizing biological and clinical diversity in lung cancers.

Out of interest, the prognostic value of these seven sub-classes was also assessed. (Note that these sub-classes were constructed based on sample staining patterns across the entire classification panel of Appendix A. This differs from the approach that was described in Example 14 where specific antibodies with predetermined prognostic value were combined into prognostic panels that were then used to classify patients). The average probability of recurrence for the overall HH cohort was first calculated and found to level out at about 38% after six years. Average probabilities within each of the seven HH sub-classes were then calculated and compared with the overall average. Sub-classes with an average probability of recurrence after six years that was greater than 48% (i.e., more than 10% worse than the overall population) were classified as having a "bad" prognosis. Sub-classes with an average probability of recurrence after six years that was less than 28% (i.e., more than 10% better than the overall population) were classified as having a "good" prognosis. Sub-classes with an average probability of recurrence after six years of 28 to 48% were classified as having a "moderate" prognosis. Based on this analysis, HH sub-classes 1, 6 and 7 were classified as "bad"; HH sub-classes 2 and 4 as "moderate"; and HH sub-classes 3 and 5 as "good". When the recurrence data for patients in the "bad", "moderate" and "good" classes were combined and plotted as Kaplan-Meier curves the different outcomes for the three prognostic groups were statistically significant (p-value <0.02, data not shown).

In order to assess whether the sub-classes of FIG. **18** would correlate across lung cancers in general, the k-means clustering criteria that were used in classifying the HH lung cohort were "forced" onto samples from an independent lung cohort (namely the UAB lung cohort that was described in Example 14). Note that while the HH lung cohort was composed of Stage I/II patients, the UAB lung cohort was composed of Stage III/IV patients. Thus, overall the prognosis of UAB patients was worse than the prognosis of HH patients. First, the mean values from the HH k-means analysis were calculated for each of the seven HH sub-classes of FIG. **18**. Antibody staining results for each UAB sample were then compared with all seven means and samples were assigned to one of the seven "HH sub-classes" based on the closest match. The seven UAB clusters were then classified as having a "bad", "moderate" and "good" prognosis based simply on the prognoses that had been previously determined for the corresponding seven HH sub-classes (see above). When the recurrence data for patients in the "bad", "moderate" and "good" classes were combined and plotted as Kaplan-Meier curves the different outcomes for the three prognostic groups were again statistically significant (p-value <0.02, data not shown). Examination of the curves and subsequent analysis showed that "good" and "moderate" gave similar outcomes relative to each other while "bad" was clearly divergent from these two.

Other Embodiments

Other embodiments of the invention will be apparent to those skilled in the art from a consideration of the specification or practice of the invention disclosed herein. It is intended that the specification and examples be considered as exemplary only, with the true scope of the invention being indicated by the following claims.

APPENDIX A

		BREAST PANEL?		LUNG PANEL?		COLON PANEL?	NCBI LocusLink	UniGene	
AGI ID	GENE NAME	Russ.	HH	Russ.	HH	Russ.	ID	ID	ALIASES
S0011	VAV-3 protein		X				10451	Hs.267659	VAV3; VAV3 ONCOGENE; ONCOGENE VAV3; vav 3 oncogene
S0018	mammoglobin		X				4250	Hs.46452	UGB2; MGB1; mammaglobin 1; MAMMAGLOBIN A PRECURSOR
S0020	RB18A (P53 binding)		X				5469	Hs.15589	RB18A; TRIP2; PPARGBP; PBP; CRSP1; PPARBP; CRSP200; DRIP230; PPAR-BINDING PROTEIN; PPARG binding protein; PPAR binding protein; CRSP, 200-KD SUBUNIT; PEROXISOME PROLIFERATOR-ACTIVATED RECEPTOR-BINDING PROTEIN; THYROID HORMONE RECEPTOR INTERACTOR 2; RECOGN
S0021	Putative cadherin-like protein	X	X	X	X		222256	Hs.12496	FLJ23834
S0022	Sim to Cyto p450	X	X	X	X	X	199974	Hs.176588	cytochrome P450 4Z1
S0024	Chuck Ras			X			85004	Hs.21594	RERG; RAS-like, estrogen-regulated, growth-inhibitor
S0032	MDGI		X				2170	Hs.49881	MDGI; O-FABP; FABP3; FABP11; H-FABP; FATTY ACID-BINDING PROTEIN, SKELETAL MUSCLE; Fatty acid-binding protein 3, muscle; fatty acid binding protein 11; FATTY ACID-BINDING PROTEIN, MUSCLE AND HEART; fatty acid binding protein 3, muscle and heart (mammary-de

APPENDIX A-continued

		BREAST PANEL?		LUNG PANEL?		COLON PANEL?	NCBI LocusLink	UniGene	
AGI ID	GENE NAME	Russ.	HH	Russ.	HH	Russ.	ID	ID	ALIASES
S0036	Human GABA-A receptor pi subunit					X	2568	Hs.70725	GABRP; GAMMA-AMINOBUTYRIC ACID RECEPTOR, PI; GABA-A RECEPTOR, PI POLYPEPTIDE; gamma-aminobutyric acid (GABA) A receptor, pi
S0037	Annexin VIII		X				244	Hs.87268	ANX8; ANXA8; annexin VIII; annexin A8
S0039	hypothetical UBCc containing protein (Ubiquitin-conjugating enzyme E2, catalytic domain homologues)	X	X	X		X		Hs.351357	
S0040	MDR1	X	X	X		X	5243	Hs.21330	GP170; PGY1; P-gp; ABCB1; ABC20; MDR1; DOXORUBICIN RESISTANCE; P-GLYCOPROTEIN 1; multidrug resistance 1; P-glycoprotein-1/multiple drug resistance-1; MULTIDRUG RESISTANCE PROTEIN 1; ATP-BINDING CASSETTE, SUBFAMILY B, MEMBER 1; P glycoprotein 1/multiple dr
S0041	MDR3	X					5244	Hs.73812	MDR2; MDR3; PGY3; PFIC-3; ABCB4; ABC21; MDR2/3; P-GLYCOPROTEIN 3; MULTIDRUG RESISTANCE 3; P-glycoprotein-3/multiple drug resistance-3; MULTIDRUG RESISTANCE PROTEIN 3; P glycoprotein 3/multiple drug resistance 3; ATP-binding cassette, sub-family B (MDR/TAP
S0042	MRP-1	X	X	X		X	4363	Hs.89433	MRP; MRP1; GS-X; ABC29; ABCC1; ABCC; multidrug resistance protein; multiple drug resistance-associated protein; MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 1; multiple drug resistance protein 1; ATP-BINDING CASSETTE, SUBFAMILY C, MEMBER 1; ATP-binding cassett
S0043	MRP2/CMOAT	X	X	X		X	1244	Hs.193852	MRP2; cMRP; CMOAT; ABCC2; ABC30; ABC#; CMOAT1; DJS; MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 2; CANALICULAR MULTIDRUG RESISTANCE PROTEIN; MULTISPECIFIC ORGANIC ANION TRANSPORTER, CANALICULAR; CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1; ATP-BINDI
S0044	MRP4	X	X	X		X	10257	Hs.139336	MOAT-B; MRP4; ABCC4; MOATB; EST170205; MRP/CMOAT-RELATED ABC TRANSPORTER; MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 4; MULTISPECIFIC ORGANIC ANION TRANSPORTER B; ATP-binding cassette, sub-family C, member 4; ATP-BINDING CASSETTE, SUBFAMILY C, MEMBER 4; ATP-
S0045	MRP3/CMOAT2	X					8714	Hs.90786	MOAT-D; MRP3; ABCC3; MLP2; ABC31; EST90757; CMOAT2; MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 3; canicular multispecific organic anion transporter; ATP-BINDING CASSETTE, SUBFAMILY C, MEMBER 3; CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 2; ATP-bindi

APPENDIX A-continued

AGI ID	GENE NAME	BREAST PANEL? Russ.	BREAST PANEL? HH	LUNG PANEL? Russ.	LUNG PANEL? HH	COLON PANEL? Russ.	NCBI LocusLink ID	UniGene ID	ALIASES
S0046	MRP5/MOAT-C	X		X	X	X	10057	Hs.108660	ABCC5; MRP5; EST277145; ABC33; SMRP; pABC11; MOATC; ABC TRANSPORTER MOAT-C; MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 5; canalicular multispecific organic anion transporter C; ATP-binding cassette, sub-family C, member 5; ATP-BINDING CASSETTE, SUBFAMILY C,
S0047	MRP6	X		X		X	368	Hs.274260	MOAT-E; MRP6; ARA; EST349056; ABCC6; MOATE; PXE; MLP1; ABC34; *pseudoxanthoma elasticum*; ANTHRACYCLINE RESISTANCE-ASSOCIATED PROTEIN; MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 6; ATP-BINDING CASSETTE, SUBFAMILY C, MEMBER 6; ATP-binding cassette, sub-family C
S0048	BSEP	X					8647	Hs.158316	BSEP; ABCB11; PFIC-2; SPGP; PGY4; PFIC2; ABC16; SISTER OF P-GLYCOPROTEIN; bile salt export pump; progressive familial intrahepatic cholestasis 2; ABC member 16, MDR/TAP subfamily; ATP-BINDING CASSETTE, SUBFAMILY B, MEMBER 11; ATP-binding cassette, sub-fam
S0049	ATP-binding cassette, sub-family B, member 10	X	X				23456	Hs.1710	MTABC2; EST20237; MABC2; M-ABC2; ABCB10; MITOCHONDRIAL ABC PROTEIN 2; ATP-BINDING CASSETTE, SUBFAMILY B, MEMBER 10; ATP-binding cassette, sub-family B, member 10; ATP-binding cassette, sub-family B (MDR/TAP), member 10
S0050	TAP1	X	X				6890	Hs.352018	
S0052	SUR1	X		X		X	6833	Hs.54470	SUR1; MRP8; ABC36; SUR; HI; ABCC8; HRINS; PHHI; sulfonylurea receptor (hyperinsulinemia); SULFONYLUREA RECEPTOR 1; SULFONYLUREA RECEPTOR, BETA-CELL HIGH-AFFINITY; ATP-binding cassette, sub-family C, member 8; ATP-BINDING CASSETTE, SUBFAMILY C, MEMBER 8; A
S0053	SUR2	X	X				10060	Hs.248960	SUR2; ABC37; ABCC9; sulfonylurea receptor 2A; ATP-BINDING CASSETTE, SUBFAMILY C, MEMBER 9; ATP-binding cassette, sub-family C (CFTR/MRP), member 9; ATP-binding cassette, sub-family C, member 9, isoform SUR2A-delta-14; ATP-binding cassette, sub-family C, m
S0055	INTEGRAL MEMBRANE PROTEIN 2B (TRANSMEMBRANE PROTEIN BRI)		X				9445	Hs.239625	E25B; ABRI; E3-16; FBD; BRI2; BRICD2B; ITM2B; BRI GENE; BRICHOS domain containing 2B; integral membrane protein 2B
S0057	ANK-3		X				288	Hs.75893	ankyrin-G; ANK3; ankyrin-3, node of Ranvier; ankyrin 3 isoform 1; ankyrin 3 isoform 2; ankyrin 3, node of Ranvier (ankyrin G)
S0058	hypothetical protein FLJ21918 (RNA recognition motif (RRM) containing protein)			X			80004	Hs.282093	FLJ21918; hypothetical protein FLJ21918
S0059	ataxia-telangiectasia group D-associated protein	X	X	X		X	23650	Hs.82237	ATDC; TRIM29; tripartite motif-containing 29; ataxia-telangiectasia group D-associated protein; tripartite motif protein TRIM29 isoform alpha; tripartite motif protein TRIM29 isoform beta

APPENDIX A-continued

		BREAST PANEL?		LUNG PANEL?		COLON PANEL?	NCBI LocusLink	UniGene	
AGI ID	GENE NAME	Russ.	HH	Russ.	HH	Russ.	ID	ID	ALIASES
S0059P2	ataxia-telangiectasia group D-associated protein		X		X		23650	Hs.82237	ATDC; TRIM29; tripartite motif-containing 29; ataxia-telangiectasia group D-associated protein; tripartite motif protein TRIM29 isoform alpha; tripartite motif protein TRIM29 isoform beta
S0063	iroquois related homeobox 3		X	X	X	X	79191	Hs.3321	
S0068	Chuck Ras C-term		X				85004	Hs.416854	RERG; hypothetical protein MGC15754; RAS-like, estrogen-regulated, growth-inhibitor
S0070	putative G protein-coupled receptor (NP_055188.1)	X					26996	Hs.97101	GPCR150; GPR160; putative G protein-coupled receptor; G protein-coupled receptor 160
S0072	Calgranulin A		X		X		6279	Hs.100000	MRP-8; MIF; S100A8; MRP8; CFAG; L1Ag; 60B8AG; P8; CGLA; CAGA; NIF; MA387; CP-10; CYSTIC FIBROSIS ANTIGEN; MIGRATION INHIBITORY FACTOR-RELATED PROTEIN 8; LEUKOCYTE L1 COMPLEX LIGHT CHAIN; S100 calcium-binding protein A8 (calgranulin A)
S0073	hepatocyte nuclear protein 3, alpha		X				3169	Hs.70604	HNF3A; MGC33105; TCF3A; FOXA1; forkhead box A1; HEPATOCYTE NUCLEAR FACTOR 3-ALPHA; hepatocyte nuclear factor 3, alpha
S0073P2	hepatocyte nuclear protein 3, alpha		X		X		3169	Hs.70604	HNF3A; MGC33105; TCF3A; FOXA1; forkhead box A1; HEPATOCYTE NUCLEAR FACTOR 3-ALPHA; hepatocyte nuclear factor 3, alpha
S0074	intestinal trefoil precursor	X	X	X		X	7033	Hs.82961	TFF3; trefoil factor 3 (intestinal); trefoil factor 3, HITF, human intestinal trefoil factor
S0074P3	intestinal trefoil precursor				X		7033	Hs.82961	TFF3; trefoil factor 3 (intestinal); trefoil factor 3, HITF, human intestinal trefoil factor
S0076x1	Keratin 17		X				3872	Hs.2785	PCHC1; PC; PC2; 39.1; KRT17; K17; CYTOKERATIN 17; VERSION 1; CK 17; KERATIN, TYPE I CYTOSKELETAL 17
S0079	LIV-1		X		X		25800	Hs.79136	LIV-1; LIV-1 protein, estrogen regulated
S0081	NAT1	X	X				9	Hs.155956	MNAT; NAT-1; AAC1; NAT1; ACETYL-CoA:ARYLAMINE N-ACETYLTRANSFERASE; EC 2.3.1.5; arylamine N-acetyltransferase-1; N-ACETYLTRANSFERASE TYPE 1; ARYLAMINE N-ACETYLTRANSFERASE, MONOMORPHIC; ARYLAMINE N-ACETYLTRANSFERASE 1; N-acetyltransferase 1 (arylamine N-ace
S0086	x-box binding		X				7494	Hs.149923	XBP2; TREB5; XBP1; X-box-binding protein-1; X BOX-BINDING PROTEIN 1; X BOX-BINDING PROTEIN 2; X-box binding protein 1
S0096	ATPase, H+ transporting, lysosomal (vacuolar proton pump), beta polypeptide, 56/58 kD, isoform 1R7340		X		X		525	Hs.64173	ATP6B1; VATB; 3.6.1.34; VPP3; RTA1B; EC 3.6.3.14; V-ATPASE B1 SUBUNIT; VACUOLAR PROTON PUMP B ISOFORM 1; ENDOMEMBRANE PROTON PUMP 58 KDA SUBUNIT; VACUOLAR ATP SYNTHASE SUBUNIT B, KIDNEY ISOFORM; ATPase, H+ TRANSPORTING, LYSOSOMAL, BETA SUBUNIT, ISOFORM 1;

APPENDIX A-continued

		BREAST PANEL?		LUNG PANEL?		COLON PANEL?	NCBI LocusLink	UniGene	
AGI ID	GENE NAME	Russ.	HH	Russ.	HH	Russ.	ID	ID	ALIASES
S0110	hypothetical protein MGC2714 (in part)	X		X		X	84259	Hs.74284	hypothetical protein MGC2714
S0117	Reproduction 8					X	7993	Hs.153678	D8S2298E; REP8; reproduction 8; Reproduction/chromosome 8
S0119	slit1					X	6585	Hs.133466	SLIT3; MEGF4; SLIL1; Slit-1; SLIT1; slit homolog 1 (Drosophila); SLIT, DROSOPHILA, HOMOLOG OF, 1; MULTIPLE EPIDERMAL GROWTH FACTOR-LIKE DOMAINS 4
S0132	sry-box9	X		X		X	6662	Hs.2316	SRA1; CMD1; SOX9; CMPD1; CMPD1 SRY-BOX 9; transcription factor SOX9; TRANSCRIPTION FACTOR SOX-9; ACAMPOMELIC CAMPOMELIC DYSPLASIA; SRY-RELATED HMG-BOX GENE 9; SEX REVERSAL, AUTOSOMAL, 1; SRY (sex-determining region Y)-box 9 protein; SRY (sex-determining r
S0137	EGF-Like Domain, Multiple 2	X	X	X	X	X	1952	Hs.57652	EGFL2; CDHF10; KIAA0279; CELSR2; MEGF3; EGF-like-domain, multiple 2; epidermal growth factor-like 2; multiple epidermal growth factor-like domains 3; cadherin EGF LAG seven-pass G-type receptor 2; similar to cadherin-related tumor suppressor hFat protein;
S0139	Gamma-glytamyl hydrolase	X	X				8836	Hs.78619	GGH; GH; EC 3.4.19.9; GAMMA-GLU-X CARBOXYPEPTIDASE; GAMMA-GLUTAMYL HYDROLASE PRECURSOR; gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase) precursor
S0140	Bullous Pemphigoid Antigen 1	X	X	X		X	667	Hs.198689	BP240; FLJ13425; FLJ32235; FLJ21489; FLJ30627; CATX-15; KIAA0728; BPAG1; dystonin; hemidesmosomal plaque protein; bullous pemphigoid antigen 1, 230/240 kDa; bullous pemphigoid antigen 1 (230/240 kD); bullous pemphigoid antigen 1 isoform 1eA precursor; bullo
S0140P1	Bullous Pemphigoid Antigen 1		X				667	Hs.198689	BP240; FLJ13425; FLJ32235; FLJ21489; FLJ30627; CATX-15; KIAA0728; BPAG1; dystonin; hemidesmosomal plaque protein; bullous pemphigoid antigen 1, 230/240 kDa; bullous pemphigoid antigen 1 (230/240 kD); bullous pemphigoid antigen 1 isoform 1eA precursor; bullo
S0143	fasn	X	X	X			2194	Hs.83190	FASN; FAS; EC 2.3.1.85; EC 4.2.1.61; EC 1.3.1.10; EC 1.1.1.100; EC 3.1.2.14; EC 2.3.1.41; EC 2.3.1.38; EC 2.3.1.39; fatty acid synthase
S0143P3	fasn		X		X		2194	Hs.83190	FASN; FAS; EC 2.3.1.85; EC 4.2.1.61; EC 1.3.1.10; EC 1.1.1.100; EC 3.1.2.14; EC 2.3.1.41; EC 2.3.1.38; EC 2.3.1.39; fatty acid synthase
S0144	Matrix Metalloproteinase 14	X		X			4323	Hs.2399	MMP-14; MMP-X1; MT1MMP; MMP14; MTMMP1; MT1-MMP; EC 3.4.24.—; MT-MMP 1; membrane-type-1 matrix metalloproteinase; MATRIX METALLOPROTEINASE-14 PRECURSOR; matrix metalloproteinase 14 (membrane-inserted); membrane-type matrix metalloproteinase 1; MATRIX METAL

APPENDIX A-continued

		BREAST PANEL?		LUNG PANEL?		COLON PANEL?	NCBI LocusLink	UniGene	
AGI ID	GENE NAME	Russ.	HH	Russ.	HH	Russ.	ID	ID	ALIASES
S0149	ABP/ZF	X					55503	Hs.302740	TRPV6; ECAC2; CAT1; CATL; CALCIUM TRANSPORTER 1; CALCIUM TRANSPORTER-LIKE PROTEIN; EPITHELIAL CALCIUM CHANNEL 2; transient receptor potential cation channel, subfamily V, member 6
S0156	fatty acid binding protein 7, FABP7	X		X		X	2173	Hs.26770	B-FABP; FABP7; FABPB; MRG; mammary-derived growth inhibitor-related; FATTY ACID-BINDING PROTEIN 7; FATTY ACID-BINDING PROTEIN, BRAIN; fatty acid binding protein 7, brain
S0158	Cadherin 3	X	X	X		X	1001	Hs.2877	CDHP; HJMD; PLACENTAL-CADHERIN; PCAD; CDH3; placental cadherin; CADHERIN-3 PRECURSOR; CADHERIN, PLACENTAL; calcium-dependent adhesion protein, placental; cadherin 3, type 1 preproprotein; cadherin 3, type 1, P-cadherin (placental); cadherin 3, P-cadherin
S0165	GRO1 Oncogene	X	X				2919	Hs.789	GRO1; CXCL1; MGSA; SCYB1; GROA; GRO PROTEIN, ALPHA; GRO1 oncogene (melanoma growth-stimulating activity); MELANOMA GROWTH STIMULATORY ACTIVITY, ALPHA; GRO1 oncogene (melanoma growth stimulating activity, alpha); SMALL INDUCIBLE CYTOKINE SUBFAMILY B, MEMBE
S0171	Effector cell protease receptor 1	X					N/A	Hs.1578	BIRC5; baculoviral IAP repeat-containing 5 (survivin)
S0193	PLOD2		X				5352	Hs.41270	PLOD2; LYSYL HYDROXYLASE 2; LYSINE HYDROXYLASE 2; PROCOLLAGEN-LYSINE, 2-OXOGLUTARATE 5-DIOXYGENASE 2; procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2; procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2 isoform
S0211	Cytochrome p450, subfamily IIa	X		X			1549	Hs.250615	CYPIIA7; P450-IIA4; CPAD; CPA7; CYP2A7; EC 1.14.14.1; CYTOCHROME P450 2A7; cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 7, isoform 2; cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 7, isoform 1
S0218	Putative nucleoside transporter-like protein	X					222962	Hs.4302	ENT4
S0221	Solute Carrier Family 28 (sodium-coupled nucleoside transporter), member 2"	X	X				9153	Hs.193665	HCNT2; SLC28A2; CNT2; SPNT1; SPNT; CNT 2; SODIUM/NUCLEOSIDE COTRANSPORTER 2; NA(+)/NUCLEOSIDE COTRANSPORTER 2; SODIUM/PURINE NUCLEOSIDE CO-TRANSPORTER; SODIUM-COUPLED NUCLEOSIDE TRANSPORTER 2; CONCENTRATIVE NUCLEOSIDE TRANSPORTER 2; SODIUM-DEPENDENT PURIN
S0223	Hepatic angiopoietin-related protein	X		X		X	51129	Hs.9613	HFARP; FIAF; ANGPTL4; PGAR; angiopoietin-like 4; FASTING-INDUCED ADIPOSE FACTOR; PPARG ANGIOPOIETIN-RELATED PROTEIN; HEPATIC FIBRINOGEN/ANGIOPOIETIN-RELATED PROTEIN; PPAR(gamma) angiopoietin related protein; PPAR(gamma) angiopoietin related gene; angiopoi

APPENDIX A-continued

		BREAST PANEL?		LUNG PANEL?		COLON PANEL?	NCBI LocusLink	UniGene	
AGI ID	GENE NAME	Russ.	HH	Russ.	HH	Russ.	ID	ID	ALIASES
S0235	Carcinoembryonic antigen-related cell adhesion molecule 5		X				1048	Hs.220529	CEA; CEACAM5; CD66e; carcinoembryonic antigen-related cell adhesion molecule 5
S0237	podocalyxin-like protein 1		X				5420	Hs.16426	PCLP; PODXL; PODOCALYXIN-LIKE PROTEIN
S0241	glycyl-tRNA synthetase	X		X		X	2617	Hs.293885	
S0251	LBP protein 32					X	29841	Hs.321264	LBP-32; LBP protein 32
S0253	Putative Integral Membrane Transporter (LC27)	X	X				55353	Hs.296398	LAPTM4beta; LC27; putative integral membrane transporter; lysosomal-associated transmembrane protein 4 beta
S0255	Cyclin E2		X	X	X	X	9134	Hs.408658	CYCE2; CCNE2; G1/S-SPECIFIC CYCLIN E2
S0260	KIAA0253		X	X	X		23385	Hs.4788	KIAA0253; nicastrin; NCSTN
S0265	FXYD domain-containing ion transport regulator 3			X		X	5349	Hs.301350	MAT-8; MAT8; PLML; FXYD3; phospholemman-like protein; MAMMARY TUMOR, 8-KD; FXYD domain-containing ion transport regulator 3; FXYD domain containing ion transport regulator 3; FXYD domain containing ion transport regulator 3 isoform 2 precursor; FXYD domai
S0267	Immunoglobulin Superfamily, Member 3			X			3321	Hs.81234	V8; IGSF3; immunoglobin superfamily, member 3; immunoglobulin superfamily, member 3
S0270	STAM2			X			10254	Hs.17200	STAM2; DKFZp564C047; Hbp; hypothetical protein; SIGNAL-TRANSDUCING ADAPTOR MOLECULE 2; STAM-like protein containing SH3 and ITAM domains 2; signal transducing adaptor molecule (SH3 domain and ITAM motif) 2
S0273	Dickkopf Homolog 1			X			22943	Hs.40499	DKK1; DKK-1; SK; dickkopf-1 like; dickkopf (*Xenopus laevis*) homolog 1; dickkopf homolog 1 (*Xenopus laevis*); DICKKOPF, *XENOPUS*, HOMOLOG OF, 1
S0280	Putative Anion Transporter 1	X					65010	Hs.298476	SLC26A6; DKFZP586E1422; solute carrier family 26, member 6
S0286	Wnt Inhibitory Factor 1		X				11197	Hs.284122	WIF1; WIF-1; Wnt inhibitory factor-1; WNT INHIBITORY FACTOR 1
S0288	PRAME			X			23532	Hs.30743	MAPE; PRAME; OPA-INTERACTING PROTEIN 4; Opa-interacting protein OIP4; preferentially expressed antigen in melanoma; melanoma antigen preferentially expressed in tumors
S0295	Prostaglandin E Synthase			X			9536	Hs.146688	PGES; TP53I12; MGST1L1; PP1294; PP102; PTGES; MGC10317; PIG12; MGST1-L1; MGST-IV; MGST1-like 1; p53-INDUCED GENE 12; prostaglandin E synthase; p53-induced apoptosis protein 12; prostaglandin E synthase isoform 2; prostaglandin E synthase isoform 1; micros
S0296	Solute Carrier Family 7, member 5/LAT1 protein	X	X	X		X	8140	Hs.184601	SLC7A5; MPE16; D16S469E; E16; 4F2LC; CD98; HLAT1; LAT1; CD98LC; 4F2 LC; 4F2 light chain; CD98 LIGHT CHAIN; INTEGRAL MEMBRANE PROTEIN E16; L-TYPE AMINO ACID TRANSPORTER 1; Solute carrier family 7, member 5; LARGE NEUTRAL AMINO ACIDS TRANSPORTER SMALL SUBUN
S0296P1	Solute Carrier Family 7, member 5/LAT1 protein		X		X		8140	Hs.184601	SLC7A5; MPE16; D16S469E; E16; 4F2LC; CD98; HLAT1; LAT1; CD98LC; 4F2 LC; 4F2 light chain; CD98 LIGHT CHAIN; INTEGRAL MEMBRANE PROTEIN E16; L-TYPE AMINO ACID TRANSPORTER 1; Solute carrier family 7, member 5; LARGE NEUTRAL AMINO ACIDS TRANSPORTER SMALL SUBUN

APPENDIX A-continued

AGI ID	GENE NAME	BREAST PANEL? Russ.	BREAST PANEL? HH	LUNG PANEL? Russ.	LUNG PANEL? HH	COLON PANEL? Russ.	NCBI LocusLink ID	UniGene ID	ALIASES
S0297	v-maf musculoaponeurotic fibrosarcoma (avian) oncogene family, protein K or NF-E2p18"			X			7975	Hs.131953	FLJ32205; NFE2U; MAFK; NFE2, 18-KD SUBUNIT; nuclear factor erythroid-2, ubiquitous (p18); NUCLEAR FACTOR ERYTHROID 2, UBIQUITOUS SUBUNIT; v-maf musculoaponeurotic fibrosarcoma oncogene homolog K (avian); v-maf avian musculoaponeurotic fibrosarcoma oncogen
S0301	CEGP1	X					57758	Hs.222399	SCUBE2; signal peptide, CUB domain, EGF-like 2
S0303	GABRE gamma-aminobutyric acid (GABA) A receptor, epsilon		X	X	X	X	2564	Hs.22785	GABRE; GABA(A) RECEPTOR; GABA-A RECEPTOR, EPSILON POLYPEPTIDE; GAMMA-AMINOBUTYRIC ACID RECEPTOR, EPSILON; GAMMA-AMINOBUTYRIC-ACID RECEPTOR EPSILON SUBUNIT PRECURSOR; gamma-aminobutyric acid (GABA) A receptor, epsilon, isoform 3; gamma-aminobutyric acid (G
S0305	S100 calcium-binding protein A10		X	X		X	6281	Hs.400250	ANX2L; p10; GP11; S100A10; 42C; ANX2LG; CAL1L; P11; CLP11; Ca[1]; P10 PROTEIN; CALPACTIN I LIGHT CHAIN; CALPACTIN I, p11 SUBUNIT; CALPACTIN I, LIGHT CHAIN; CELLULAR LIGAND OF ANNEXIN II; S100 calcium-binding protein A10 (annexin II ligand, calpactin I, li
S0311	v-myb avian myeloblastosis viral oncogene homolog-like 2	X		X		X	4605	Hs.179718	MYBL2; MGC15600; MYB-RELATED GENE BMYB; MYB-related protein B; v-myb myeloblastosis viral oncogene homolog (avian)-like 2; V-MYB AVIAN MYELOBLASTOSIS VIRAL ONCOGENE HOMOLOG-LIKE 2
S0312	nucleoside phosphorylase	X					4860	Hs.75514	PNP; NP; EC 2.4.2.1; INOSINE PHOSPHORYLASE; PURINE-NUCLEOSIDE:ORTHOPHOSPHATE RIBOSYLTRANSFERASE; purine nucleoside phosphorylase; PNP NUCLEOSIDE PHOSPHORYLASE DEFICIENCY; ATAXIA WITH DEFICIENT CELLULAR IMMUNITY
S0314	aldo-keto reductase family 1, member C4			X		X	22948	Hs.1600	KIAA0098; CCT5; chaperonin containing TCP1, subunit 5 (epsilon)
S0315	Non-metastatic cells 1, protein (NM23A)	X	X	X		X	4830	Hs.118638	NM23H1; NDPKA; NM23; NM23-H1; NME1; NDK A; EC 2.7.4.6; NUCLEOSIDE DIPHOSPHATE KINASE-A; NDP KINASE A; METASTASIS INHIBITION FACTOR NM23; NUCLEOSIDE DIPHOSPHATE KINASE A; non-metastatic cells 1 protein; TUMOR METASTATIC PROCESS-ASSOCIATED PROTEIN; NONMETAS
S0316	Squalene epoxidase	X	X	X			6713	Hs.71465	SQLE; SE; ERG1; EC 1.14.99.7; squalene epoxidase; squalene monooxygenase
S0319	Pregnancy-induced growth inhibitor			X			29948	Hs.31773	OKL38; pregnancy-induced growth inhibitor
S0326	Putative 4TM Mal-like protein	X		X		X	114569	Hs.76550	MAL2; MAL proteolipid protein 2; mal, T-cell differentiation protein 2

APPENDIX A-continued

AGI ID	GENE NAME	BREAST PANEL? Russ.	BREAST PANEL? HH	LUNG PANEL? Russ.	LUNG PANEL? HH	COLON PANEL? Russ.	NCBI LocusLink ID	UniGene ID	ALIASES
S0330	aldo-keto reductase family 1, member C1/C2			X	X	X	1645	Hs.306098	DDH1; 2-ALPHA-HSD; MBAB; 20-ALPHA-HSD; H-37; DD1; DD2; HBAB; AKR1C1; HAKRC; DDH; EC 1.3.1.20; 20 ALPHA-HYDROXYSTEROID DEHYDROGENASE; ALDO-KETO REDUCTASE C; DIHYDRODIOL DEHYDROGENASE 2; DIHYDRODIOL DEHYDROGENASE, TYPE I; CHLORDECONE REDUCTASE HOMOLOG HAKRC
S0330x1	aldo-keto reductase family 1, member C1/C2			X	X		1645	Hs.306098	DDH1; 2-ALPHA-HSD; MBAB; 20-ALPHA-HSD; H-37; DD1; DD2; HBAB; AKR1C1; HAKRC; DDH; EC 1.3.1.20; 20 ALPHA-HYDROXYSTEROID DEHYDROGENASE; ALDO-KETO REDUCTASE C; DIHYDRODIOL DEHYDROGENASE 2; DIHYDRODIOL DEHYDROGENASE, TYPE I; CHLORDECONE REDUCTASE HOMOLOG HAKRC
S0331	aldo-keto reductase family 1, member C3			X	X		8644	Hs.78183	HA1753; DD3; PGFS; HAKRB; KIAA0119; 3ALPHA-HSD; DDH1; AKR1C3; EC 1.3.1.20; 3-ALPHA-HYDROXYSTEROID DEHYDROGENASE; PROBABLE TRANS-1,2-DIHYDROBENZENE-1,2-DIOL DEHYDROGENASE; ALDO-KETO REDUCTASE B; DIHYDRODIOL DEHYDROGENASE 3; PROSTAGLANDIN F SYNTHASE; 3-@ALP
S0331x1	aldo-keto reductase family 1, member C3			X	X		8644	Hs.78183	HA1753; DD3; PGFS; HAKRB; KIAA0119; 3ALPHA-HSD; DDH1; AKR1C3; EC 1.3.1.20; 3-ALPHA-HYDROXYSTEROID DEHYDROGENASE; PROBABLE TRANS-1,2-DIHYDROBENZENE-1,2-DIOL DEHYDROGENASE; ALDO-KETO REDUCTASE B; DIHYDRODIOL DEHYDROGENASE 3; PROSTAGLANDIN F SYNTHASE; 3-@ALP
S0332	aldo-keto reductase family 1, member C4			X	X		1645	Hs.306098	1.1.1.213; 2-ALPHA-HSD; 1.3.1.20; 20-ALPHA-HSD; MGC8954; H-37; HAKRC; MBAB; C9; DDH1; AKR1C1; trans-1,2-dihydrobenzene-1,2-diol dehydrogenase; chlordecone reductase homolog; aldo-keto reductase C; 20 alpha-hydroxysteroid dehydrogenase; hepatic dihydrodiol
S0332x1	aldo-keto reductase family 1, member C4			X	X		1645	Hs.306098	1.1.1.213; 2-ALPHA-HSD; 1.3.1.20; 20-ALPHA-HSD; MGC8954; H-37; HAKRC; MBAB; C9; DDH1; AKR1C1; trans-1,2-dihydrobenzene-1,2-diol dehydrogenase; chlordecone reductase homolog; aldo-keto reductase C; 20 alpha-hydroxysteroid dehydrogenase; hepatic dihydrodiol
S0336	Putative ParB-like nuclease domain containing protein			X			140809	Hs.135056	
S0342	Putative glucose transporter-like protein	X	X	X		X	154091	Hs.26691	GLUT8; GLUT12
S0343	Putative glucose transporter-like protein	X	X	X			154091	Hs.26691	GLUT8; GLUT12
S0374	chloride intracellular channel 5 (CLIC5),	X		X		X	53405	Hs.283021	CLIC5; chloride intracellular channel 5
S0380	hypothetical protein (AX119005 Sequence 169 from Patent WO0129221)			X				Hs.59509	

APPENDIX A-continued

		BREAST PANEL?		LUNG PANEL?		COLON PANEL?	NCBI LocusLink	UniGene	
AGI ID	GENE NAME	Russ.	HH	Russ.	HH	Russ.	ID	ID	ALIASES
S0384	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived) (FARP1)					X	10160	Hs.183738	CDEP; FARP1; chondrocyte-derived ezrin-like protein; CHRONDROCYTE-DERIVED EZRIN-LIKE PROTEIN; FERM, RhoGEF, and pleckstrin domain protein 1; FERM, ARHGEF, AND PLECKSTRIN DOMAIN-CONTAINING PROTEIN 1; FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (c
S0388	zinc finger transcription factor TRPS1 (trichorhinophalangeal syndrome I gene)	X					7227	Hs.26102	TRPS1; TRICHORHINOPHALANGEAL SYNDROME GENE; trichorhinophalangeal syndrome I gene; ZINC FINGER TRANSCRIPTION FACTOR TRPS1
S0398	FAT tumor suppressor (*Drosophila*) homolog (FAT)		X	X	X		2195	Hs.166994	ME5; CDHF7; FAT; cadherin ME5; FAT PROTEIN HOMOLOG; FAT tumor suppressor precursor; FAT tumor suppressor (*Drosophila*) homolog; cadherin-related tumor suppressor homolog precursor; cadherin family member 7 precursor; homolog of *Drosophila* Fat protein precu
S0401	granulin (GRN)			X		X	2896	Hs.180577	ACROGRANIN; PROEPITHELIN; PROGRANULIN; PEPI; PCDGF; granulin; GRN; EPITHELIN PRECURSOR
S0404	N-myc downstream regulated (NDRG1)	X	X	X	X	X	10397	Hs.75789	NDR1; DRG1; RTP; NDRG1; RIT42; CAP43; NDRG1 PROTEIN; DIFFERENTIATION-RELATED GENE 1 PROTEIN; NICKEL-SPECIFIC INDUCTION PROTEIN CAP43; NMYC DOWNSTREAM-REGULATED GENE 1; REDUCING AGENTS AND TUNICAMYCIN-RESPONSIVE PROTEIN; N-MYC DOWNSTREAM REGULATED GENE 1 P
S0411	fatty acid binding protein 5 (psoriasis-associated)(FABP5)			X			2171	Hs.380942	PAFABP; EFABP; E-FABP; FABP5; PA-FABP; FATTY ACID-BINDING PROTEIN, EPIDERMAL; FATTY ACID-BINDING PROTEIN 5; FATTY ACID-BINDING PROTEIN, PSORIASIS-ASSOCIATED; fatty acid binding protein 5 (psoriasis-associated)
S0413	cyclin-dependent kinase inhibitor 1C (p57, Kip2)(CDKN1C)			X			1028	Hs.106070	WBS; p57(KIP2); BWCR; CDKN1C; BWS; Beckwith-Wiedemann syndrome; cyclin-dependent kinase inhibitor 1C (p57, Kip2)
S0414	alpha-methylacyl-CoA racemase(AMACR)					X	23600	Hs.128749	AMACR; 5.1.99.4; ALPHA-METHYLACYL-CoA RACEMASE; AMACR DEFICIENCY; AMACR ALPHA-METHYLACYL-CoA RACEMASE DEFICIENCY; alpha-methylacyl-CoA racemase isoform 1; alpha-methylacyl-CoA racemase isoform 2
S0415	gamma-aminobutyric acid (GABA) A receptor, beta 3(GABRB3)	X	X				2562	Hs.1440	MGC9051; GABRB3; GABA-A RECEPTOR, BETA-3 POLYPEPTIDE; GAMMA-AMINOBUTYRIC ACID RECEPTOR, BETA-3; gamma-aminobutyric acid (GABA) A receptor, beta 3; gamma-aminobutyric acid (GABA) A receptor, beta 3 isoform 2 precursor; gamma-aminobutyric acid (GABA) A rece

APPENDIX A-continued

		BREAST PANEL?		LUNG PANEL?		COLON PANEL?	NCBI LocusLink	UniGene	
AGI ID	GENE NAME	Russ.	HH	Russ.	HH	Russ.	ID	ID	ALIASES
S0417	KIAA0872 protein (KIAA0872)	X	X				22879	Hs.436089	KIAA0872 protein
S0425	tumor necrosis factor receptor superfamily, member 21(TNFRSF21)					X	27242	Hs.159651	TNFRSF21; DR6; BM-018; TNFR-related death receptor 6; tumor necrosis factor receptor superfamily, member 21; tumor necrosis factor receptor superfamily, member 21 precursor
S0429	KIAA1380 (thyroid hormone receptor interactor 8)(TRIP8)					X	221037	Hs.381298	JMJD1C; TRIP8; jumonji domain containing 1C; THYROID HORMONE RECEPTOR INTERACTOR 8
S0432	BSTP5	X		X	X	X		Hs.19322	
S0440	cell division cycle 25B (cdc25b)	X	X				994	Hs.153752	CDC25HU2; EC 3.1.3.48; M-PHASE INDUCER PHOSPHATASE 2; DUAL SPECIFICITY PHOSPHATASE CDC25B; cell division cycle 25B, isoform 4; cell division cycle 25B, isoform 1; cell division cycle 25B, isoform 2; cell division cycle 25B, isoform 3
S0445	laminin, beta 1 (lamb1)			X			3912	Hs.82124	LAMB1; LAMININ, BETA-1; CUTIS LAXA-MARFANOID SYNDROME; laminin, beta 1; laminin, beta 1 precursor; LAMB1 NEONATAL CUTIS LAXA WITH MARFANOID PHENOTYPE
S0447	papillary renal cell carcinoma (translocation-associated) (prcc)	X					5546	Hs.9629	TPRC; MGC17178; MGC4723; PRCC; proline-rich protein PRCC; RCCP1 PRCC/TFE3 FUSION GENE; papillary renal cell carcinoma (translocation-associated); RENAL CELL CARCINOMA, PAPILLARY, 1 GENE; papillary renal cell carcinoma translocation-associated gene product
S0455	tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10)					X	8743	Hs.83429	APO2L; TL2; Apo-2L; TNFSF10; Apo-2 ligand; APO2 LIGAND; TNF-RELATED APOPTOSIS-INDUCING LIGAND; TNF-related apoptosis inducing ligand TRAIL; tumor necrosis factor (ligand) superfamily, member 10; TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY, MEMBER 10
S0459	titin	X	X				7273	Hs.434384	titin; CMH9; TTN; TTN CARDIOMYOPATHY, FAMILIAL HYPERTROPHIC, 9
S0469	DNA fragmentation factor, 45 kD, alpha polypeptide			X			1676	Hs.105658	DFF45; DFF1; DFFA; ICAD; DFF-45; INHIBITOR OF CASPASE-ACTIVATED DNase; DNA FRAGMENTATION FACTOR, 45-KD, ALPHA SUBUNIT; DNA fragmentation factor, 45 kDa, alpha polypeptide; DNA fragmentation factor, 45 kD, alpha subunit; DNA fragmentation factor, 45 kD, alp
S0494	Caspase 2	X					835	Hs.108131	CASP-2; ICH-1L/1S; CASP2; ICH1; NEDD2; CASPASE-2 PRECURSOR; ICH-1 protease; EC 3.4.22.—; NEDD2 apoptosis regulatory gene; caspase 2, isoform 3; caspase 2, isoform 4; caspase 2, isoform 1 preproprotein; caspase 2, isoform 2 precursor; NEURAL PRECURSOR CELL
S0501	G1 to S phase transition 1 (GSPT1)	X		X		X	2935	Hs.2707	GSPT1; eRF3a; ETF3A; GST1, YEAST, HOMOLOG OF; PEPTIDE CHAIN RELEASE FACTOR 3A; G1-TO S-PHASE TRANSITION 1; G1 to S phase transition 1

APPENDIX A-continued

		BREAST PANEL?		LUNG PANEL?		COLON PANEL?	NCBI LocusLink	UniGene	
AGI ID	GENE NAME	Russ.	HH	Russ.	HH	Russ.	ID	ID	ALIASES
S0502	GCN5 general control of amino-acid synthesis 5-like 2 (yeast) (GCN5L2)	X		X		X	2648	Hs.101067	hGCN5; GCN5; GCN5L2; HSGCN5; EC 2.3.1.—; HISTONE ACETYLTRANSFERASE GCN5; GENERAL CONTROL OF AMINO ACID SYNTHESIS PROTEIN 5-LIKE 2; GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 2; General control of amino acid synthesis, yeast, homol
S0507	Guanylate-binding protein (FLJ23293)			X			64225	Hs.27099	ARL6IP2; ADP-ribosylation factor-like 6 interacting protein 2
S0511	HSPC037 protein	X					51659	Hs.433180	Pfs2; DNA replication complex GINS protein PSF2
S0524	Hypothetical protein (FLJ20093)	X					55608	Hs.172572	ANKRD10; ankyrin repeat domain 10
S0527	Hypothetical protein (KIAA0176)					X	N/A	Hs.4935	KCTD2; potassium channel tetramerisation domain containing 2
S0528	Hypothetical protein (KIAA0856)	X		X			23312	Hs.13264	RC3; KIAA0856; rabconnectin-3
S0544	RhoGEF containing hypothetical protein (FLJ14642)	X					84904	Hs.245342	hypothetical protein FLJ14642
S0545	RNA methyltransferase (Hpall tiny fragments locus 9C)	X	X		X		27037	Hs.63609	D22S1733E; HTF9C; Hpall tiny fragments locus 9C; Hpall tiny fragments locus 9C
S0546	Serine rich hypothetical protein	X					157313	Hs.373547	CDCA2; cell division cycle associated 2
S0553	Similar to mitotic phosphoprotein 44 [*Xenopus laevis*]			X		X		Hs.180591	
S0557	SMC4 (structural maintenance of chromosomes 4, yeast)-like 1; SMC4L1; CAP-C					X	10051	Hs.50758	CAP-C; SMC4L1; CAPC; HCAP-C; chromosome-associated polypeptide C; SMC4 (structural maintenance of chromosomes 4, yeast)-like 1; structural maintenance of chromosomes (SMC) family member, chromosome-associated protein C
S0564	phosphatidylserine synthase 1	X	X	X		X	9791	Hs.77329	KIAA0024; PSSA; PTDSS1; EC 2.7.8.—; phosphatidylserine synthase 1; PHOSPHATIDYLSERINE SYNTHASE I (SERINE-EXCHANGE ENZYME I) (EC 2.7.8.—)
S0565	polo (*Drosophia*)-like kinase	X	X				5347	Hs.433619	PLK1; PLK; PLK-1; STPK13; POLO-LIKE KINASE; EC 2.7.1.—; polo (*Drosophia*)-like kinase; SERINE/THREONINE-PROTEIN KINASE PLK; SERINE-THREONINE PROTEIN KINASE 13; SERINE THREONINE PROTEIN KINASE 13
S0567	Pirin	X				X	8544	Hs.424966	Pirin; PIR
S0578	ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3)			X			21	Hs.26630	ABCA3; ABC3; LBM180; ABC-C; EST111653; ABC transporter 3; ATP-binding cassette 3; ATP-BINDING CASSETTE TRANSPORTER 3; ATP-BINDING CASSETTE, SUBFAMILY A, MEMBER 3; ATP-binding cassette, sub-family A member 3; ATP-binding cassette, sub-family A (ABC1), memb
S0579	ATP-binding cassette, sub-family A (ABC1), member 7 (ABCA7)			X	X		10347	Hs.134514	ABCX; ABCA7; ABCA-SSN; autoantigen SS-N; macrophage ABC transporter; ATP-BINDING CASSETTE, SUBFAMILY A, MEMBER 7; ATP-binding cassette, sub-family A (ABC1), member 7; ATP-binding cassette, sub-family A, member 7, isoform a; ATP-binding cassette, sub-famil

APPENDIX A-continued

AGI ID	GENE NAME	BREAST PANEL? Russ.	BREAST PANEL? HH	LUNG PANEL? Russ.	LUNG PANEL? HH	COLON PANEL? Russ.	NCBI LocusLink ID	UniGene ID	ALIASES
S0581	ATP-binding cassette, sub-family B (MDR/TAP), member 7 (ABCB7)		X	X		X	22	Hs.125856	ABCB7; Atm1p; ASAT; ABC7; EST140535; ABC TRANSPORTER 7; ATP-binding cassette 7; ATP-BINDING CASSETTE TRANSPORTER 7; Anemia, sideroblastic, with spinocerebellar ataxia; ATP-BINDING CASSETTE, SUBFAMILY B, MEMBER 7; ATP-binding cassette, sub-family B, member
S0585	ATP-binding cassette, sub-family C (CFTR/MRP), member 12 (ABCC12)			X		X	94160	Hs.343663	MRP9; ABCC12; ATP-binding cassette, sub-family C, member 12; ATP-binding cassette, sub-family C (CFTR/MRP), member 12
S0586	ATP-binding cassette, sub-family G (WHITE), member 2 (ABCG2)			X	X		9429	Hs.194720	ABC15; MXR1; ABCP; EST157481; MXR; ABCG2; ABC1; BCRP; mitoxantrone resistance protein; breast cancer resistance protein; placenta specific MDR protein; ATP-BINDING CASSETTE TRANSPORTER, PLACENTA-SPECIFIC; ATP-BINDING CASSETTE, SUBFAMILY G, MEMBER 2; ATP-b
S0593	solute carrier family 21 (organic anion transporter), member 8 (SLC21A8)	X	X	X		X	28234	Hs.274981	SLC21A8; OATP8; ORGANIC ANION TRANSPORTER 8; SOLUTE CARRIER FAMILY 21, MEMBER 8; solute carrier family 21 (organic anion transporter), member 8
S0597	solute carrier family 22 (organic anion transporter), member 6 (SLC22A6)	X					9356	Hs.23965	ROAT1; MGC45260; HOAT1; PAHT; SLC22A6; PAH TRANSPORTER; para-aminohippurate transporter; renal organic anion transporter 1; solute carrier family 22 member 6 isoform b; solute carrier family 22 member 6 isoform c; solute carrier family 22 member 6 isoform
S0604	solute carrier family 35 (UDP-galactose transporter), member 2 (SLC35A2)	X		X		X	7355	Hs.21899	UGT2; UGTL; UGAT; SLC35A2; UGT1; UDP-galactose translocator; UDP-GALACTOSE TRANSPORTER, ISOFORM 2; UGALT UDP-GALACTOSE TRANSPORTER, ISOFORM 1; solute carrier family 35 (UDP-galactose transporter), member A2; solute carrier family 35 (UDP-galactose transpo
S0607	cdc25b isoforms 1,3					X	994	Hs.153752	CDC25HU2; EC 3.1.3.48; M-PHASE INDUCER PHOSPHATASE 2; DUAL SPECIFICITY PHOSPHATASE CDC25B; cell division cycle 25B, isoform 4; cell division cycle 25B, isoform 1; cell division cycle 25B, isoform 2; cell division cycle 25B, isoform 3
S0609	SCD stearoyl-CoA desaturase delta-9-desaturase		X				6319	Hs.119597	SCD; DELTA(9)-DESATURASE; ACYL-COA DESATURASE; EC 1.14.99.5; stearoyl-CoA desaturase (delta-9-desaturase); FATTY ACID DESATURASE
S0611	MAPK12 mitogen-activated protein kinase 12		X		X		6300	Hs.55039	SAPK3; p38gamma; SAPK-3; ERK6; MAPK12; p38-GAMMA; PRKM12; ERK-6; ERK3; ERK5; EC 2.7.1.—; STRESS-ACTIVATED PROTEIN KINASE-3; mitogen-activated protein kinase 3; EXTRACELLULAR SIGNAL-REGULATED KINASE 6; MAP KINASE P38 GAMMA; stress-activated protein kinase

APPENDIX A-continued

AGI ID	GENE NAME	BREAST PANEL? Russ.	BREAST PANEL? HH	LUNG PANEL? Russ.	LUNG PANEL? HH	COLON PANEL? Russ.	NCBI LocusLink ID	UniGene ID	ALIASES
S0612	NFKB2 nuclear factor of kappa light 2 (p49/p100)			X		X	4791	Hs.73090	LYT-10; LYT10; NFKB2; ONCOGENE LYT 10; TRANSCRIPTION FACTOR NFKB2; NFKB, p52/p100 SUBUNIT; LYMPHOCYTE TRANSLOCATION CHROMOSOME 10; NUCLEAR FACTOR KAPPA-B, SUBUNIT 2; Nuclear factor of kappa light chain gene enhancer in B-cells 2; nuclear factor of kappa I
S0613	TNFRSF5: tumor necrosis factor receptor superfamily, member 5 (CD40)			X		X	958	Hs.25648	Bp50; TNFRSF5; MGC9013; CDW40; CD40 antigen; CD40L receptor; B CELL-ASSOCIATED MOLECULE CD40; CD40 type II isoform; B cell surface antigen CD40; nerve growth factor receptor-related B-lymphocyte activation molecule; tumor necrosis factor receptor superfam
S0614	EBI3 Epstein-Barr virus induced gene 3		X	X	X		10148	Hs.185705	EBI3; EPSTEIN-BARR VIRUS-INDUCED GENE 3; Epstein-Barr virus induced gene 3 precursor
S0616	ZNF339: zinc finger protein 339		X				58495	Hs.71935	ZNF339; zinc finger protein 339
S0617	DAB2IP: DAB2 interacting protein	X					153090	Hs.238465	DAB2IP; DAB2 interacting protein
S0618	PPFIA1: protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1					X	8500	Hs.183648	MGC26800; LIP1; PPFIA1; LIP.1; LAR-interacting protein 1; PTPRF interacting protein alpha 1 isoform a; PTPRF interacting protein alpha 1 isoform b; protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1
S0631	hypothetical protein CAB66760					X	56963	Hs.271277	RGMA; REPULSIVE GUIDANCE MOLECULE; RGM domain family, member A
S0633	novel hypothetical protein	X				X	144347	Hs.432901	LOC144347; hypothetical protein LOC144347
S0645	frizzled homolog 7 FZD7		X				8324	Hs.173859	FzE3; FZD7; frizzled 7; frizzled homolog 7 (*Drosophila*); Frizzled, *drosophila*, homolog of, 7
S0646	SLC3A2: solute carrier family 3, member 2	X	X				6520	Hs.79748	MDU1; 4T2HC; SLC3A2; NACAE; 4F2HC; 4F2 HEAVY CHAIN; CD98 HEAVY CHAIN; CD98 MONOCLONAL ANTIBODY 44D7; ANTIGEN DEFINED BY MONOCLONAL ANTIBODY 4F2, HEAVY CHAIN; antigen identified by monoclonal antibodies 4F2, TRA1.10, TROP4, and T43; SOLUTE CARRIER FAMILY 3
S0651	PLA2R1 phospholipase A2 receptor 1					X	22925	Hs.171945	PLA2IR; PLA2-R; PLA2R1; PLA2G1R; PHOSPHOLIPASE A2 RECEPTOR, 180-KD; phospholipase A2 receptor 1, 180 kDa
S0654	KIAA0182 protein (KIAA0182)	X					23199	Hs.222171	KIAA0182; KIAA0182 protein
S0659	thymidine kinase 2, mitochondrial	X					7084	Hs.274701	TK2; THYMIDINE KINASE, MITOCHONDRIAL; thymidine kinase 2, mitochondrial
S0663	hypothetical protein FLJ12799 (FLJ12799)	X	X			X	64430	Hs.413671	FLJ12799; hypothetical protein FLJ12799
S0665	KIAA1007 protein (KIAA1007)	X	X			X	23019	Hs.279949	KIAA1007; KIAA1007 protein; adrenal gland protein AD-005; KIAA1007 protein isoform a; KIAA1007 protein isoform b
S0670	DKFZP566O1646 protein (DC8)	X					25936	Hs.24427	DC8; DKFZP566O1646 protein

APPENDIX A-continued

		BREAST PANEL?		LUNG PANEL?		COLON PANEL?	NCBI LocusLink	UniGene	
AGI ID	GENE NAME	Russ.	HH	Russ.	HH	Russ.	ID	ID	ALIASES
S0673	ART-4 protein (ART-4)		X				28987	Hs.3566	ART-4; NOB1P; adenocarcinoma antigen recognized by T lymphocytes 4; likely ortholog of mouse nin one binding protein
S0676	guanine nucleotide binding protein (G protein) alpha 12 (GNA12)		X				2768	Hs.182874	RMP; NNX3; GNA12; G alpha 12; Guanine nucleotide-binding protein, alpha-12 subunit; guanine nucleotide binding protein (G protein) alpha 12
S0677	GrpE-like protein cochaperone (HMGE)		X				80273	Hs.151903	HMGE; GrpE-like protein cochaperone; HUMAN MITOCHONDRIAL GrpE PROTEIN; GrpE, *E. COLI*, HOMOLOG OF
S0684	FLJ34922		X				91607	Hs.235709	
S0687	hypothetical protein FLJ20457		X				54942	Hs.29276	FLJ20457; hypothetical protein FLJ20457
S0691	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11				X		23657	Hs.6682	CCBR1; SLC7A11; xCT; cystine/glutamate transporter; SYSTEM Xc(—) TRANSPORTER-RELATED PROTEIN; SOLUTE CARRIER FAMILY 7, MEMBER 11; solute carrier family 7, (cationic amino acid transporter, y+ system) member 11
S0695	Integrin, beta 4		X				3691	Hs.85266	GP150; ITGB4; CD104 antigen; INTEGRIN, BETA-4; Integrin beta-4 precursor; integrin, beta 4
S0702	Solute Carrier Family 7, member 5/LAT1 protein		X		X		8140	Hs.184601	SLC7A5; MPE16; D16S469E; E16; 4F2LC; CD98; HLAT1; LAT1; CD98LC; 4F2 LC; 4F2 light chain; CD98 LIGHT CHAIN; INTEGRAL MEMBRANE PROTEIN E16; L-TYPE AMINO ACID TRANSPORTER 1; Solute carrier family 7, member 5; LARGE NEUTRAL AMINO ACIDS TRANSPORTER SMALL SUBUN
S5002	cytokeratin 14	X		X		X	3861	Hs.355214	CK; KRT14; K14; EBS4; EBS3; cytokeratin 14; CK 14; KERATIN, TYPE I CYTOSKELETAL 14; keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner)
S5003	cytokeratin 17	X					3872	Hs.514738	PCHC1; PC; PC2; 39.1; KRT17; K17; CYTOKERATIN 17; VERSION 1; CK 17; KERATIN, TYPE I CYTOSKELETAL 17
S5004	cytokeratin 18	X					3875	Hs.406013	K18; CYK18; KRT18; CYTOKERATIN 18; CK 18; KERATIN, TYPE I CYTOSKELETAL 18
S5005	CAM5.2 (cytokeratin 8/18)	X		X		X	3875	Hs.65114	K18; CYK18; KRT18; CYTOKERATIN 18; CK 18; KERATIN, TYPE I CYTOSKELETAL 18
S5012	EpCAM (Ab-1), mono	X		X		X	4072	Hs.692	TROP1; LY74; Ep-CAM; GA733-2; EGP40; MK-1; CO17-1A; EPCAM; M4S1; KSA; TACSTD1; EGP; MK-1 antigen; EPITHELIAL CELLULAR ADHESION MOLECULE; GASTROINTESTINAL TUMOR-ASSOCIATED ANTIGEN 2, 35-KD GLYCOPROTEIN; tumor-associated calcium signal transducer 1 precurso
S5014	Estrogen Receptor Beta (Ab-2), mono	X					2100	Hs.103504	ER-BETA; ESR-BETA; ESR2; Erb; ESRB; NR3A2; ESTROGEN RECEPTOR, BETA; estrogen receptor 2 (ER beta)
S5038	milk fat globule protein (C-Mu1)	X		X		X	4582	Hs.89603	PEMT; MUC1; episialin; EMA; PUM; H23AG; CD227; PEM; CARCINOMA-ASSOCIATED MUCIN; H23 antigen; TUMOR-ASSOCIATED MUCIN; DF3 antigen; peanut-reactive urinary mucin; mucin 1, transmembrane; polymorphic epithelial mucin; MUCIN 1, URINARY; MUCIN, TUMOR-ASSOCIATE

APPENDIX A-continued

AGI ID	GENE NAME	BREAST PANEL? Russ.	BREAST PANEL? HH	LUNG PANEL? Russ.	LUNG PANEL? HH	COLON PANEL? Russ.	NCBI LocusLink ID	UniGene ID	ALIASES
S5044	CD 71 MAB-3	X		X		X	7037	Hs.77356	P90; TR; TFRC; TFR; CD71; T9; TRFR; ANTIGEN CD71; TRANSFERRIN RECEPTOR PROTEIN; transferrin receptor (p90, CD71)
S5045	c-ErbB2/Her-2	X				X	2064	Hs.323910	HER-2; ERBB2; NGL; P185ERBB2; HER2; C-ERBB-2; NEU; MLN 19; EC 2.7.1.112; TKR1 HERSTATIN; NEU PROTO-ONCOGENE; ONCOGENE ERBB2; RECEPTOR PROTEIN-TYROSINE KINASE ERBB-2 PRECURSOR; ONCOGENE NGL, NEUROBLASTOMA- OR GLIOBLASTOMA-DERIVED; TYROSINE KINASE-TYPE CELL
S5047	LRP/MVP MAB-2	X		X		X	9961	Hs.80680	MVP; LRP; VAULT1; LUNG RESISTANCE-RELATED PROTEIN; MAJOR VAULT PROTEIN, RAT, HOMOLOG OF
S5064	TP63			X			8626	Hs.137569	LMS; TP73L; KET; SHFM4; p73H; EEC3; TP63; p51; TUMOR PROTEIN p63; TUMOR PROTEIN p73-LIKE; p53-RELATED PROTEIN p63; tumor protein 63 kDa with strong homology to p53
S5065	estrogen receptor 1	X					2099	Hs.1657	ER; NR3A1; ESR1; Era; ESR; ER-ALPHA; ESRA; ESTRADIOL RECEPTOR; ESTROGEN RECEPTOR, ALPHA; estrogen receptor 1 (alpha)
S5066	c-ErbB2/Her-2	X				X	2064	Hs.446352	HER-2; ERBB2; NGL; P185ERBB2; HER2; C-ERBB-2; NEU; MLN 19; EC 2.7.1.112; TKR1 HERSTATIN; NEU PROTO-ONCOGENE; ONCOGENE ERBB2; RECEPTOR PROTEIN-TYROSINE KINASE ERBB-2 PRECURSOR; ONCOGENE NGL, NEUROBLASTOMA- OR GLIOBLASTOMA-DERIVED; TYROSINE KINASE-TYPE CELL
S5067	Cathepsin D	X		X		X	1509	Hs.343475	CTSD; MGC2311; CPSD; EC 3.4.23.5; cathepsin D preproprotein; Cathepsin D precursor; cathepsin D (lysosomal aspartyl protease);
S5069	CA 125			X			94025	Hs.432676	
S5070	CA 15-3	X		X		X	N/A	N/A	
S5071	CA 19-9	X		X		X	N/A	N/A	
S5072	c-myc			X		X	4609	Hs.79070	c-Myc; MYC; ONCOGENE MYC; Myc proto-oncogene protein; PROTOONCOGENE HOMOLOGOUS TO MYELOCYTOMATOSIS VIRUS; v-myc myelocytomatosis viral oncogene homolog (avian); v-myc avian myelocytomatosis viral oncogene homolog; Avian myelocytomatosis viral (v-myc) onco
S5073	e-cadherin	X		X		X	999	Hs.194657	CDH1; Cadherin-1; Arc-1; ECAD; CDHE; Uvomorulin; LCAM; Epithelial-cadherin precursor; cell-CAM 120/80; CADHERIN, EPITHELIAL; calcium-dependent adhesion protein, epithelial; cadherin 1, E-cadherin (epithelial); cadherin 1, type 1 preproprotein; cadherin 1,
S5074	gst-pi			X		X	2950	Hs.226795	GSTP1; DFN7; GSTP1-1; GST3; GSTPP; GST class-pi; glutathione transferase; EC 2.5.1.18; glutathione S-transferase pi; GST, CLASS PI; deafness, X-linked 7; GLUTATHIONE S-TRANSFERASE 3; GLUTATHIONE S-TRANSFERASE, PI; FAEES3 GLUTATHIONE S-TRANSFERASE PI PSEUD

APPENDIX A-continued

		BREAST PANEL?		LUNG PANEL?		COLON PANEL?	NCBI LocusLink	UniGene	
AGI ID	GENE NAME	Russ.	HH	Russ.	HH	Russ.	ID	ID	ALIASES
S5075	p53			X		X	7157	Hs.1846	p53; TP53; TRP53; PHOSPHOPROTEIN P53; TRANSFORMATION-RELATED PROTEIN 53; TUMOR SUPPRESSOR P53; CELLULAR TUMOR ANTIGEN P53; tumor protein p53 (Li-Fraumeni syndrome)
S5076	progesterone receptor	X				X	5241	Hs.2905	NR3C3; PR; PGR; PROGESTERONE RESISTANCE; PSEUDOCORPUS LUTEUM INSUFFICIENCY PROGESTERONE RECEPTOR
S5077	ps2 MAB-1	X					7031	Hs.350470	
S5079	NSE	X		X		X	2026	Hs.511915	NSE; ENO2; 2-phospho-D-glycerate hydro-lyase; ENOLASE, GAMMA; neurone-specific enolase; ENOLASE, NEURON-SPECIFIC; 2-phospho-D-glycerate hydrolyase; EC 4.2.1.11; Neural enolase; enolase-2, gamma, neuronal; neuron specific gamma enolase; enolase 2, (gamma,
S5080	bcl-2			X			596	Hs.79241	BCL2; FOLLICULAR LYMPHOMA; APOPTOSIS REGULATOR BCL-2; B-cell CLL/lymphoma 2; B-cell lymphoma protein 2 alpha; B-cell lymphoma protein 2 beta; ONCOGENE B-CELL LEUKEMIA 2 LEUKEMIA, CHRONIC LYMPHATIC, TYPE 2
S5081	RB			X		X	5925	Hs.75770	p105-Rb; PP110; Retinoblastoma-1; RB; RB1; RETINOBLASTOMA-ASSOCIATED PROTEIN; RB OSTEOSARCOMA, RETINOBLASTOMA-RELATED; retinoblastoma 1 (including osteosarcoma)
S5082	Synaptophysin			X		X	6855	Hs.75667	SYP; Synaptophysin; Major synaptic vesicle protein P38
S5083	bax					X	581	Hs.159428	BAX; BCL2-associated X protein; APOPTOSIS REGULATOR BAX, MEMBRANE ISOFORM ALPHA
S6001	estrogen receptor		X				2099	Hs.1657	ER; NR3A1; ESR1; Era; ESR; ER-ALPHA; ESRA; ESTRADIOL RECEPTOR; ESTROGEN RECEPTOR, ALPHA; estrogen receptor 1 (alpha)
S6002	progesterone receptor		X				5241	Hs.2905	NR3C3; PR; PGR; PROGESTERONE RESISTANCE; PSEUDOCORPUS LUTEUM INSUFFICIENCY PROGESTERONE RECEPTOR
S6003	c-ErbB2/Her-2		X				2064	Hs.323910	HER-2; ERBB2; NGL; P185ERBB2; HER2; C-ERBB-2; NEU; MLN 19; EC 2.7.1.112; TKR1 HERSTATIN; NEU PROTO-ONCOGENE; ONCOGENE ERBB2; RECEPTOR PROTEIN-TYROSINE KINASE ERBB-2 PRECURSOR; ONCOGENE NGL, NEUROBLASTOMA- OR GLIOBLASTOMA-DERIVED; TYROSINE KINASE-TYPE CELL
S6004	bcl-2				X		596	Hs.79241	BCL2; FOLLICULAR LYMPHOMA; APOPTOSIS REGULATOR BCL-2; B-cell CLL/lymphoma 2; B-cell lymphoma protein 2 alpha; B-cell lymphoma protein 2 beta; ONCOGENE B-CELL LEUKEMIA 2 LEUKEMIA, CHRONIC LYMPHATIC, TYPE 2

APPENDIX A-continued

AGI ID	GENE NAME	BREAST PANEL? Russ.	BREAST PANEL? HH	LUNG PANEL? Russ.	LUNG PANEL? HH	COLON PANEL? Russ.	NCBI LocusLink ID	UniGene ID	ALIASES
S6005	cytokeratin 5/6		X		X		3852	Hs.433845	KRT5; EBS2; Keratin-5; K5; CYTOKERATIN 5; CK 5; 58 KDA CYTOKERATIN; KERATIN, TYPE II CYTOSKELETAL 5; keratin 5 (epidermolysis bullosa simplex, Dowling-Meara/Kobner/Weber-Cockayne types)
S6006	p53		X		X		7157	Hs.1846	p53; TP53; TRP53; PHOSPHOPROTEIN P53; TRANSFORMATION-RELATED PROTEIN 53; TUMOR SUPPRESSOR P53; CELLULAR TUMOR ANTIGEN P53; tumor protein p53 (Li-Fraumeni syndrome)
S6007	ki67		X		X		4288	Hs.80976	ki67; MKI67
S6008	EGFR 1		X		X		1956	Hs.77432	S7; EGFR; 2.7.1.112; ERBB; ONCOGENE ERBB; ERBB1 SPECIES ANTIGEN 7; V-ERB-B AVIAN ERYTHROBLASTIC LEUKEMIA VIRAL ONCOGENE HOMOLOG; epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)
S6011	NSE				X		2026	Hs.146580	NSE; ENO2; 2-phospho-D-glycerate hydro-lyase; ENOLASE, GAMMA; neurone-specific enolase; ENOLASE, NEURON-SPECIFIC; 2-phospho-D-glycerate hydrolyase; EC 4.2.1.11; Neural enolase; enolase-2, gamma, neuronal; neuron specific gamma enolase; enolase 2, (gamma,
S6012	Thyroid Transcription Factor-1				X		7080	Hs.94367	benign chorea; chorea, hereditary benign; NK-2 (*Drosophila*) homolog A (thyroid nuclear factor); Thyroid transcription factor 1 (NK-2, *Drosophila*, homolog of, A); BCH; BHC; TEBP; TTF1; NKX2A; TTF-1; NKX2.1
S6013	c-ErbB2/Her-2				X		2064	Hs.323910	HER-2; ERBB2; NGL; P185ERBB2; HER2; C-ERBB-2; NEU; MLN 19; EC 2.7.1.112; TKR1 HERSTATIN; NEU PROTO-ONCOGENE; ONCOGENE ERBB2; RECEPTOR PROTEIN-TYROSINE KINASE ERBB-2 PRECURSOR; ONCOGENE NGL, NEUROBLASTOMA- OR GLIOBLASTOMA-DERIVED; TYROSINE KINASE-TYPE CELL

	Antibody Generation				IHC Images (Appendix B)		
AGI ID	Peptide 1 (SEQ ID NO:)	Peptide 2 (SEQ ID NO:)	Peptide 3 (SEQ ID NO:)	TITER	Breast IHC	Lung IHC	Colon IHC
S0011	DYISKSKEDVKLK (1)	EKRTNGLRRTPKQVD (2)	TEESINDEDIYKGLPDLIDE (3)	1:90-1:100			
S0018	SKTINPQVSKTEYKELLQE (4)	DDNATTNAIDELKEC (5)	NQTDETLSNVEVFMQ (6)	1:300			
S0020	SSDDGIRPLPEYSTEKHKK (7)	NKTKKKKSSRLPPEK (8)	DGKSKDKPPKRKKADTE (9)	1:100			
S0021	KNKEPLTKKGETKTAERD (10)	KLTCTDLDSSPRSFRYS (11)	EVDYENPSNLAAGNKYT (12)	1:200-1:2500	2_25_2_5_66_21_58		
S0022	KTLQVFNPLRFSRENSEKIH (13)	QHFAIIECKVAVALT (14)	RKFLAPDHSRPPQPVRQ (15)	1:50-1:500	1_25_12_6_67_22_73	1_26_5_2_72_22_24	1_32_14_2_89_22_15
S0024	VLPLKNILDEIKKPKN (16)	YELCREVRRRRMVQGKT (17)	MAKSAEVKLAIFGRAGVGK (18)	1:900-1:1000			
S0032	KNTEISFKLGVEFDE (19)	HLQKWDGQETTLVRE (20)	TKPTTIIEKNGDILTLKTH (21)	1:225			
S0036	LQQMAAKDRGTTKEVEEVS (22)	KRKISFASIEISSDNVDYSD (23)	DGNDVEFTWLRGNDSVRGLEH (24)	1:250-1:500			
S0037	QRQQIAKSFKAQFGKDLTE (25)	REIMKAYEEDYGSSLEEDIQ (26)	EEYEKIANKSIEDSIKSE (27)	1:30-1:40			
S0039	EGGSLVPAARQQHCTQVRSRR (28)	RKAGKSKKSFSRKEAE (29)	KTHEKYGWVTPPVSDG (30)	1:50-1:30000	3_18_4_3_108_39_26	3_26_6_4_67_39_51	
S0040	MDLEGDRNGGAKKKN (31)	NLEDLMSNITNRSDINDTG (32)	RGSQAQDRKLSTKEA (33)	1:200-1:400	3_18_4_6_63_40_63	2_26_3_5_129_40_59	1_32_6_3_105_40_34
S0041	MDLEAAKNGTAWRPTSAE (34)	NFSFPVNFSLSLLNPGK (35)	KNSQMCQKSLDVETDG (36)	1:60-1:300	2_18_7_4_102_41_54		

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	Antibody Generation				IHC Images (Appendix B)		
AGI ID	Peptide 1 (SEQ ID NO:)	Peptide 2 (SEQ ID NO:)	Peptide 3 (SEQ ID NO:)	TITER	Breast IHC	Lung IHC	Colon IHC
S0042	MALRGFCSADGSD (37)	KNWKKECAKTRKQPVK (38)	DSIERRPVKDGGGTNS (39)	1:40-1:500	1_18_11_3_65_42_33	2_26_3_5_176_42_59	4_32_8_6_170_42_77
S0043	MLEKFCNSTFWNSSFLDSPE (40)	SILCGTFQFQTLIRT (41)	ENNESSNNPSSIAS (42)	1:50-1:333	1_18_11_3_66_43_33	3_26_12_8_177_43_101	4_32_8_6_171_43_77
S0044	QEVKPNPLQDANICSR (43)	DEISQRNRQLPSDGKK (44)	VQDFTAFWDKASETPTLQ (45)	1:20-1:100	2_18_7_10_67_44_144	2_26_8_3_169_44_36	4_32_8_6_167_44_77
S0045	MDALCGSGELGSKFWDSN (46)	RKQEKQTARHKASAA (47)	DPQSVERKTISPG (48)	1:2000			
S0046	MKDIDIGKEYIIPSPGYRS (49)	RDREDSKFRRTRPLECQD (50)	SKHESSDVNCRRLER (51)	1:100-1:300	1_18_5_5_68_46_49	1_26_14_8_134_46_99	4_32_8_6_120_46_77
S0047	MAAPAEPCAGQGVWNQTEPE (52)	DPGVVDSSSSGSAAGKD (53)	HTLVAENAMNAEK (54)	1:50	3_25_5_3_118_47_33	3_26_10_4_173_47_47	4_32_8_6_169_47_77
S0048	QEVLSKIQHGHTIIS (55)	TNSSLNQNMTNGTR (56)	MSDSVILRSIKKFGEEND (57)	1:600			
S0049	GADDPSSVTAEEIQR (58)	NAVASPEFPPRFNT (59)	KPNGIYRKLMNKQSFISA (60)	1:10-1:25	2_18_3_8_71_49_118		
S0050	MASSRCPAPRGCR (61)	QGGSGNPVRR (62)	EFVGDGIYNNTMGHVHS (63)	1:80	3_18_11_7_103_50_77		
S0052	MPLAFCGSENHSAAYR (64)	DHLGKENDVFQPKTQFLG (65)	EIREEQCAPHEPTPQG (66)	1:25-1:150	1_18_2_8_74_52_87		
S0053	MSLSFCGNNISS (67)	QRVNETQNGTNNTTGISE (68)	DEIGDDSWRTGESSLPFES (69)	1:25-1:50	3_18_3_7_75_53_69		
S0055	MVKVTFNSALAQKEAKKDEPK (70)	QTIEENIKIFEEEEVE (71)	HDKETYKLQRRETIKGIQKRE (72)	1:450-1:500			
S0057	HKKETESDQDDEIEKTDRRQ (73)	EGFKVKTKKEIRHVEKKSHS (74)	MAHAASQLKKNRDLEINAEE (75)	1:750			
S0058	ERALAAAQRCHKKVMKER (76)	TAGMKDLLSVFQAYQ (77)	DPPRTVLQAPKEWVCL (78)	1:20			

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	Antibody Generation				IHC Images (Appendix B)		
AGI ID	Peptide 1 (SEQ ID NO:)	Peptide 2 (SEQ ID NO:)	Peptide 3 (SEQ ID NO:)	TITER	Breast IHC	Lung IHC	Colon IHC
S0059	MEAADASRSN GSSPEARDAR (79)	ELHLKPHLEGAAFRDH Q (80)	EGEGLGQSLGNFK DDLLN (81)	1:50-1:3000	2_18_2_5_41_59_62	2_26_13_1_128_59_13	4_32_8_6_166_59_77
S0059P2	ELHLKPHLEG AAFRDHQ (82)	N/A	N/A	1:90			
S0063	GSEERGAGR GSSGGREE (83)	KIWSLAETATSPDNPRR S (84)	KKLLKTAFQPVPR RPQNHLD (85)	1:200-1:1200			
S0068	RRSSTTHVKQ AINKMLTKISS (86)	N/A	N/A	1:500-1:40000			
S0070	MRRKNTCQNF MEYFCISLAF (87)	NETILYFPFSSHSSYTV RSKK (88)	KVQIPAYIEMNIPL VILCQ (89)	1:10-1:100			
S0072	MLTELEKALN SIIDVYHK (90)	RDDLKKLLETECPQYIR KKGAD (91)	KMGVAAHKKSHE ESHKE (92)	1:6500-1:10000			
S0073	PESRKDPSGA SNPSADS (93)	HGLAPHESQLHLKGD (94)	EQQHKLDFKAYEQ ALQYS (95)	1:100-1:2700			
S0073P2	PESRKDPSGA SNPSADS (96)	HGLAPHESQLHLKGD (97)	EQQHKLDFKAYEQ ALQYS (98)	1:50-1:450			
S0074	EEYVGLSANQ CAVPAKDRVD (99)	RVDCGYPHVTPKECN (100)	VPWCFKPLQEAEC TF (101)	1:2500-1:30000	1_25_8_4_98_74_49	2_26_4_3_68_74_32	
S0074P3	VPWCFKPLQE AECTF (102)	N/A	N/A	1:810			
S0076x1	KKEPVTTRQV RTIVEE (103)	QDGKVISSREQVHQTT R (104)	SSSIKGSSGLGGG SS (105)	1:200			
S0079	DHNHAASGKN KRKALCPDHD (106)	EEPAMEMKRGPLFSHL SSQNI (107)	QRYSREELKDAGV ATL (108)	1:400-1:800			
S0081	MDIEAYLERIG YKKSRNKLDL E (109)	QMWQPLELISGKDQPQ VPCVFR (110)	FNISLQRKLVPKH GDRFFTI (111)	1:10-1:60	1_18_5_5_55_81_49		

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	Antibody Generation				IHC Images (Appendix B)		
AGI ID	Peptide 1 (SEQ ID NO:)	Peptide 2 (SEQ ID NO:)	Peptide 3 (SEQ ID NO:)	TITER	Breast IHC	Lung IHC	Colon IHC
S0086	QPPFLCQWG RHQPSWKPL MN (112)	EKTHGLVVENQELRQR LGMD (113)	RQRLTHLSPEEKA LRRKLKNR (114)	1:180-1:400			
S0096	REHMQAVTRN YITHPR (115)	KKSKAVLDYHDDN (116)	DEFYSREGRLQDL APDTAL (117)	1:100-1:800			
S0110	RYAFDFARDK DQRSLDID (118)	SVFYQYLEQSKYRVMN KDQ (119)	EDGAWPVLLDEFV EWQKVRQTS (120)	1:500-1:2500	1_25_14_7_92_110_98	1_26_4_7_207_110_88	4_32_8_6_207_110_77
S0117	SFKSPQVYLK EEEEKNEKR (121)	RKKQQEAQGEKASRYI E (122)	EDIGITVDTVLILEE KEQTN (123)	1:200			
S0119	DFRCEEGQEE GGCLPRPQ (124)	DGTSFAEEVEKPTKCG CALCA (125)	KAFRGATDLKNLR LDKNQ (126)	1:900			
S0132	MNLLDPFMKM TDEQEKGLS (127)	NTFPKGEPDLKKESEE DK (128)	KNGQAEAEEATEQ THISPN (129)	1:100-1:500	4_25_6_1_95_132_6	1_26_4_8_127_132_109	
S0137	QASSLRLEPG RANDGDWH (130)	ELKGFAERLQRNESGL DSGR (131)	RSGKSQPSYIPFLL REE (132)	1:2000-1:5000	4_25_14_3_51_137_42	1_26_3_1_65_137_3	1_32_5_3_80_137_33
S0139	RRSDYAKVAK IFYNLSIQSFD D (133)	KNFTMNEKLKKFFNVLT TN (134)	EFFVNEARKNNHH FKSESEE (135)	1:2500-1:30000			
S0140	KNTQAAEALV KLYETKLCE (136)	QENQPENSKTLATQLN Q (137)	KQMEKDLAFQKQ VAEKQLK (138)	1:250-1:20000	2_25_5_5_70_140_61		
S0140P1	KNTQAAEALV KLYETKLCE (136)	N/A	N/A	1:270			
S0143	EFVEQLRKEG VFAKEVR (139)	DRHPQALEAAQAELQQ HD (140)	REVRQLTLRKLQE LSSKADE (141)	1:5000-1:30000	2_25_12_8_64_143_101		
S0143P3	EFVEQLRKEG VFAKEVR (139)	DRHPQALEAAQAELQQ HD (140)	REVRQLTLRKLQE LSSKADE (141)	1:300-1:630			

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	Antibody Generation				IHC Images (Appendix B)		
AGI ID	Peptide 1 (SEQ ID NO:)	Peptide 2 (SEQ ID NO:)	Peptide 3 (SEQ ID NO:)	TITER	Breast IHC	Lung IHC	Colon IHC
S0144	AYIREGHEKQ ADIMIFFAE (142)	DEASLEPGYPKHIKELG R (143)	RGSFMGSDEVFTY FYK (144)	1:500-1:20000	2_25_13_7_54_144_97	2_26_12_7_208_144_96	
S0149	RQEHCMSEHF KNRPACLGAR (145)	QGHKWGESPSQGTQA GAGK (146)	RACGKRVSEGDR NGSGGGKWG (147)	1:400-1:20000			
S0156	MVEAFCATWK LTNSQN (148)	QVGNVTKPTVIISQE (149)	KVVIRTLSTFKNTE (150)	1:100-1:20000			
S0158	RAVFREAEVT LEAGGAEQE (151)	QEPALFSTDNDDFTVR N (152)	QKYEAHVPENAVG HE (153)	1:150-1:500	1_18_9_10_8_158_102	1_26_3_8_69_158_110	1_32_2_1_94_158_2
S0165	KKIIEKMLNSD KSN (154)	N/A	N/A	1:100-1:500			
S0171	GKPGNQNSK NEPPKKRERE R (155)	QAEAPLVPLSRQNK (156)	NCFLTERKAQPDE (157)	1:22500-1:30000			
S0193	KQVDLENVWL DFIRE (158)	EFDTVDLSAVDVHPN (159)	NKEVYHEKDIKVFF DKAK (160)	1:20000			
S0211	KRGIEERIQEE SGFLIE (161)	DRVIGKNRQPKFEDRT K (162)	NPQHFLDDKGQFK KSD (163)	1:500-1:2500			
S0218	RHCILGEWLPI LIMAVFN (164)	KQRELAGNTMTVSYMS (165)	RNAHGSCLHASTA NGSILAGL (166)	1:20-1:50	4_25_8_5_73_218_64		
S0221	ELMEKEVEPE GSKRTD (167)	KARSFCKTHARLFKK (168)	KNKRLSGMEEWIE GEK (169)	1:500-1:1200			
S0223	EGSTDLPLAP ESRVDPE (170)	KVAQQQRHLEKQHLR (171)	DHKHLDHEVAKPA RRKRLPE (172)	1:30-1:10000		1_32_8_3_135_223_36	
S0235	KLTIESTPFNV AEGKEC (173)	KSDLVNEEATGQFRVY PELPK (174)	KPVEDKDAVAFTC EPEAQ (175)	1:500-1:4500			
S0237	DEKLISLICRA VKATFNPAQD K (176)	KDKWDELKEAGVSDM KLGD (177)	DSWIVPLDNLTKD DLDEEEDTHL (178)	1:1000			

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	Antibody Generation				IHC Images (Appendix B)		
AGI ID	Peptide 1 (SEQ ID NO:)	Peptide 2 (SEQ ID NO:)	Peptide 3 (SEQ ID NO:)	TITER	Breast IHC	Lung IHC	Colon IHC
S0241	RKRVLEAKEL ALQPKDDIVD (179)	RHGVSHKVDDSSGSIG RRYAR (180)	EARYPLFEGQETG KKETIEE (181)	1:500-1:7500		1_26_7_3_133_241_35	4_32_8_6_168_241_77
S0251	EALYPQRRSY TSEDEAWK (182)	DYYKVPRERRSSTAKP EVE (183)	DKYDVPHDKIGKIF KKCKK (184)	1:5400			2_32_5_6_134_251_80
S0253	DPDQYNFSSS ELGGDFEFMD D (185)	EYIRQLPPNFPYRDD (186)	DTTVLLPPYDDAT VNGAAKE (187)	1:500-1:2000			
S0255	RREEVTKKHQ YEIR (188)	KESRYVHDKHFEVLHS DLE (189)	DFFDRFMLTQKDI NK (190)	1:1000-1:2000			
S0260	ESKHFTRDLM EKLKGRTSR (191)	ETDRLPRCVRSTARLA R (192)	ESRWKDIRARIFLI ASKELE (193)	1:3600-1:5400			
S0265	SEWRSSGEQ AGR (194)	KCKCKFGQKSGHHPG E (195)	KVTLGLLVFLAGFP VLDANDLED (196)	1:400			
S0267	KVAKESDSVF VLKIYHLRQED (197)	EREKTVTGEFIDKESKR PK (198)	KRAEDTAGQTALT VMRPD (199)	1:200-1:250		2_26_9_1_205_267_9	
S0270	KVARKVRALY DFEAVEDNE (200)	ETEVAAVDKLNVIDDDV E (201)	EIKKSEPEPVYIDE DKMDR (202)	1:1000-1:9000		2_26_8_3_200_270_36	
S0273	DEECGTDEYC ASPTRGGD (203)	RGEIEETITESFGNDHS TLD (204)	N/A	1:400-1:500			
S0280	MDLRRRDYH MERPLLNQEH LEE (205)	DTDIYRDVAEYSEAKE (206)	EFYSDALKQRCGV DVDFLISQKKK (207)	1:1800-1:2400	2_25_6_1_108_280_6		
S0286	DAHQARVLIG FEEDILIVSE (208)	ERRICECPDGFHGPHC EK (209)	N/A	1:90			
S0288	DIKMILKMVQL DSIEDLE (210)	KRKVDGLSTEAEQPFIP VE (211)	KEGACDELFSYLIE KVKRKK (212)	1:1200			
S0295	RLRKKAFANP EDALR (213)	RSDPDVERCLRAHRND (214)	RVAHTVAYLGKLR APIR (215)	1:100-1:2400			

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	Antibody Generation				IHC Images (Appendix B)		
AGI ID	Peptide 1 (SEQ ID NO:)	Peptide 2 (SEQ ID NO:)	Peptide 3 (SEQ ID NO:)	TITER	Breast IHC	Lung IHC	Colon IHC
S0296	KRRALAAPAA EEKEEAR (216)	EAREKMLAAKSADGSA PAGE (217)	MIWLRHRKPELER PIK (218)	1:300-1:5000	1_25_8_4_56_296_49	3_26_13_6_54_296_72	4_32_8_6_90_296_77
S0296P1	KRRALAAPAA EEKEEAR (216)	EAREKMLAAKSADGSA PAGE (217)	MIWLRHRKPELER PIK (218)	1:225-1:1350			
S0297	KPNKALKVKK EAGE (219)	KRVTQKEELERQRVEL QQEVEK (220)	RLELDALRSKYE (221)	1:333-1:800			
S0301	KMHTDGRSCL EREDTVLEVT E (222)	KKGFKLLTDEKSCQDV DE (223)	KRTEKRLRKAIRTL RKAVHRE (224)	1:3500-1:5400			
S0303	RVEGPQTESK NEASSRD (225)	EETKSTETETGSRVGKL PE (226)	N/A	1:300			
S0305	DKGYLTKEDL RVLMEKE (227)	KDPLAVDKIMKDLDQC RDGK (228)	N/A	1:8300-1:10000			
S0311	EEDLKEVLRS EAGIELIIEDDI R (229)	MSRRTRCEDLDELHYQ DTDSD (230)	RRSPIKKVRKSLAL DIVDED (231)	1:750-1:5000			
S0312	EDYKNTAEWL LSHTKHR (232)	DERFGDRFPAMSDAYD RTMRQR (233)	KVIMDYESLEKAN HEE (234)	1:1000-1:3600			
S0314	DQDRKSRLM GLEALKSHIMA AK (235)	KGVIVDKDFSHPQMPK KVED (236)	RMILKIDDIRKPGE SEE (237)	1:6000-1:30000			
S0315	RLQPEFKPKQ LEGTMANCER (238)	KFMQASEDLLKEHYVD LKDR (239)	DSVESAEKEIGLW FHPEELVD (240)	1:9000-1:18000	1_18_2_4_16_315_43	2_26_8_3_206_315_36	
S0316	KSPPESENKE QLEARRRR (241)	RDGRKVTVIERDLKEPD R (242)	DHLKEPFLEATDN SHLR (243)	1:1000-1:10000	1_25_12_1_85_316_12	2_26_3_3_75_316_31	
S0319	DLEVKDWMQ KKRRGLRNSR (244)	EYHKVHQMMREQSILS PSPYEGYR (245)	RHQLLCFKEDCQA VFQDLEGVEK (246)	1:900		2_26_6_6_203_319_79	

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	Antibody Generation				IHC Images (Appendix B)		
AGI ID	Peptide 1 (SEQ ID NO:)	Peptide 2 (SEQ ID NO:)	Peptide 3 (SEQ ID NO:)	TITER	Breast IHC	Lung IHC	Colon IHC
S0326	GPDILRTYSGA FVCLE (247)	CSLGLALRRWRP (248)	N/A	1:120-1:1200	2_25_8_1_42_326_8		3_32_12_4_115_326_45
S0330	RYLTLDIFAGP PNYPFSDEY (249)	N/A	N/A	1:2500-1:75000		4_27_11_1_140_330_11	3_32_7_2_78_330_22
S0330x1	RYLTLDIFAGP PNYPFSDEY (249)	N/A	N/A	1:600			
S0331	HYFNSDSFAS HPNYPYSDEY (250)	N/A	N/A	1:300-1:320		2_26_5_5_59_331_29	
S0331x1	HYFNSDSFAS HPNYPYSDEY (250)	N/A	N/A	1:150			
S0332	RYVVMDFLMD HPDYPFSDEY (251)	N/A	N/A	1:400		2_26_5_5_60_332_61	
S0332x1	RYVVMDFLMD HPDYPFSDEY (251)	N/A	N/A	1:100-1:150			
S0336	DPAKVQSLVD TIREDPD (252)	RETIPAKLVQSTLSDLR (253)	N/A	1:1600			
S0342	SDTTEELTVIK SSLKDE (254)	N/A	N/A	1:400-1:1250	3_25_12_8_111_342_101	3_26_8_3_132_342_36	
S0343	HSRSSLMPLR NDVDKR (255)	N/A	N/A	1:50-1:125	2_18_13_6_30_343_78		
S0374	DANTCGEDKG SRRKFLDGDE (256)	N/A	N/A	1:5000-1:9000	2_25_2_4_109_374_55		
S0380	QLEEMTELES PKCKRQENEQ (257)	N/A	N/A	1:2000-1:9000		2_26_8_7_195_380_92	
S0384	QADGAASAPT EEEEEVVKDR (258)	N/A	N/A	1:100			

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	Antibody Generation				IHC Images (Appendix B)		
AGI ID	Peptide 1 (SEQ ID NO:)	Peptide 2 (SEQ ID NO:)	Peptide 3 (SEQ ID NO:)	TITER	Breast IHC	Lung IHC	Colon IHC
S0388	SGDSLETKED QKMSPKATEE (259)	N/A	N/A	1:600			
S0398	KIRLPEREKPD RERNARREP (260)	N/A	N/A	1:200			
S0401	RGTKCLRREA PRWDAPLRDP (261)	N/A	N/A	1:600-1:2000			
S0404	GTRSRSHTSE GTRSRSHTSE (262)	N/A	N/A	1:100-1:900	4_18_8_4_9_404_53	2_26_5_5_66_404_61	4_32_8_6_91_404_77
S0411	EETTADGRKT QTVCNFTD (263)	N/A	N/A	1:1800			
S0413	AKRKRSAPEK SSGDVP (264)	N/A	N/A	1:2700			
S0414	RVDRPGSRYD VSRLGRGKRS (265)	N/A	N/A	1:100			
S0415	ETVDKLLKGY DIRLRPD (266)	N/A	N/A	1:600-1:1800			
S0417	APGGAEDLED TQFPSEEARE (267)	N/A	N/A	1:9000			
S0425	RKSSRTLKKG PRQDPSAIVE (268)	N/A	N/A	1:9000			
S0429	GSESGDSDES ESKSEQRTKR (269)			1:1200			
S0432	EADSGDARRL PRARGERRR H (270)	N/A	N/A	1:90-1:100	2_25_11_6_50_432_74	4_26_1_3_209_432_29	2_32_7_1_209_432_7

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	Antibody Generation				IHC Images (Appendix B)		
AGI ID	Peptide 1 (SEQ ID NO:)	Peptide 2 (SEQ ID NO:)	Peptide 3 (SEQ ID NO:)	TITER	Breast IHC	Lung IHC	Colon IHC
S0440	RLERPQDRDT PVQNKRRRS (271)	N/A	N/A	1:350-1:1200	1_18_11_6_249_440_56		
S0445	DRVEDVMME RESQFKEKQE (272)	N/A	N/A	1:600			
S0447	DEAFKRLQGK RNRGREE (273)	N/A	N/A	1:6000			
S0455	RFQEEIKENTK NDKQ (274)	N/A	N/A	1:900			
S0459	KRDKEGVRW TKCNKKTLTD (275)	N/A	N/A	1:2700-1:8100			
S0469	KEGSLLSKQE ESKAAFGEE (276)			1:600			
S0494	ESDAGKEKLP KMRLPTRSD (277)	N/A	N/A	1:2000			
S0501	ERDKGKTVEV GRAYFETEK (278)	N/A	N/A	1:15000			
S0502	EKFRVEKDKL VPEKR (279)	N/A	N/A	1:9000			
S0507	ENYEDDDLVN SDEVMKKP (280)	N/A	N/A	1:9000			
S0511	PKADEIRTLVK DMWDTR (281)	N/A	N/A	1:2000			
S0524	RKRCLEDSED FGVKKARTE (282)	N/A	N/A	1:4500			

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	Antibody Generation				IHC Images (Appendix B)		
AGI ID	Peptide 1 (SEQ ID NO:)	Peptide 2 (SEQ ID NO:)	Peptide 3 (SEQ ID NO:)	TITER	Breast IHC	Lung IHC	Colon IHC
S0527	EPKSFLCRLC CQEDPELDS (283)	N/A	N/A	1:1500			
S0528	EEYDRESKSS DDVDYRGS (284)	N/A	N/A	1:350-1:1200			
S0544	EQRARWERK RACTARE (285)	N/A	N/A	1:40			
S0545	ERKQLECEQV LQKLAKE (286)	N/A	N/A	1:900-1:5400			
S0546	RNSETKVRRS TRLQKDLEN (287)	N/A	N/A	1:1200			
S0553	SDYQVISDRQ TPKKDE (288)	N/A	N/A	1:5400			
S0557	DIEGKLPQTE QELKE (289)	N/A	N/A	1:200			
S0564	DDVNYKMHFR MINEQQVED (290)	N/A	N/A	1:1000-1:8000	3_25_5_3_45_564_33		
S0565	ENPLPERPRE KEEPVVR (291)	N/A	N/A	1:10-1:100	2_18_15_5_99_565_75		
S0567	REQSEGVGA RVRRSIGRPE (292)	N/A	N/A	1:240			
S0578	PRAVAGKEEE DSDPEKALR (293)			1:1500			
S0579	EKADTDMEGS VDTRQEK (294)	N/A	N/A	1:400			

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	Antibody Generation				IHC Images (Appendix B)		
AGI ID	Peptide 1 (SEQ ID NO:)	Peptide 2 (SEQ ID NO:)	Peptide 3 (SEQ ID NO:)	TITER	Breast IHC	Lung IHC	Colon IHC
S0581	RVQNHDNPK WEAKKENISK (295)	N/A	N/A	1:4000-1:10000			
S0585	RSPPAKGATG PEEQSDSLK (296)	N/A	N/A	1:500			
S0586	REEDFKATEII EPSKQDKP (297)	N/A	N/A	1:333-1:400			
S0593	DKTCMKWST NSCGAQ (298)	N/A	N/A	1:500-1:2400			
S0597	DANLSKNGGL EVWL (299)	N/A	N/A	1:3000			
S0604	EPFLPKLLTK (300)	N/A	N/A	1:2400			
S0607	RKSEAGSGAA SSSGEDKEN (301)	N/A	N/A	1:1800			
S0609	DDIYDPTYKD KEGPSPKVE (302)	N/A	N/A	1:2000-1:5000			
S0611	QSDEAKNNM KGLPELEKKD (303)	N/A	N/A	1:100			
S0612	SRPQGLTEAE QRELEQEAK (304)	N/A	N/A	1:4500			
S0613	RVQQKGTSET DTIC (305)	N/A	N/A	1:250-1:270			
S0614	VRLSPLAERQ LQVQWE (306)	N/A	N/A	1:1200-1:3000			
S0616	RRSLGVSVRS WDELPDEKR (307)	N/A	N/A	1:2500			

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	Antibody Generation				IHC Images (Appendix B)		
AGI ID	Peptide 1 (SEQ ID NO:)	Peptide 2 (SEQ ID NO:)	Peptide 3 (SEQ ID NO:)	TITER	Breast IHC	Lung IHC	Colon IHC
S0617	DEGLGPDPPH RDRLRSK (308)	N/A	N/A	1:600			
S0618	SGKRSSDGSL SHEEDLAK (309)	N/A	N/A	1:150			
S0631	SQERSDSPEI CHYEKSFHK (310)	N/A	N/A	1:600			
S0633	KVNPEPTHEIR CNSEVK (311)	N/A	N/A	1:100-1:200			
S0645	SDGRGRPAFP FSCPRQ (312)	N/A	N/A	1:900			
S0646	GSKEDFDSLL QSAKK (313)	N/A	N/A	1:3600-1:5400			
S0651	QKEEKTWHEA LRSCQADN (314)	N/A	N/A	1:3600			
S0654	EKAEEGPRKR EPAPLDK (315)	N/A	N/A	1:400			
S0659	EQNRDRILTPE NRK (316)			1:300			
S0663	RDWYIGLVSD EKWK (317)	N/A	N/A	1:900			
S0665	DSYLKTRSPV TFLSDLR (318)			1:1500-1:3000			
S0670	KCRGETVAKE ISEAMKS (319)	N/A	N/A	1:900			
S0673	KPPQETEKGH SACEPEN (320)			1:50			

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	Antibody Generation				IHC Images (Appendix B)		
AGI ID	Peptide 1 (SEQ ID NO:)	Peptide 2 (SEQ ID NO:)	Peptide 3 (SEQ ID NO:)	TITER	Breast IHC	Lung IHC	Colon IHC
S0676	ERRAGSGAR DAERE (321)	N/A	N/A	1:1200			
S0677	SEQKADPPAT EKTLLE (322)	N/A	N/A	1:500-1:1000			
S0684	EAEWSQGVQ GTLRIKKYLT (323)	N/A	N/A	1:8100			
S0687	EESKSITEGLL TQKQYE (324)			1:1260			
S0691	QNFKDAFSGR DSSITR (325)	N/A	N/A	1:1575-1:2000			
S0695	TEDVDEFRNK LQGER (326)	N/A	N/A	1:4050			
S0702	KGDVSNLDPN FSFEGTKLDV (327)	N/A	N/A	1:133650-1:178200			

APPENDIX C

BREAST PROGNOSIS (HH COHORT)			All Log rank		ER Pos Log rank		ER Pos/ Node Neg Log rank		ER neg Log rank	
AGI ID	Dilution (1:X)	Scoring method	P value	Hazard ratio	P value	Hazard ratio	P value	Hazard ratio	P value	Hazard ratio
s0021	500	3	0.0001	2.8378	0.0014	3.6147	0.0003	4.9455	0.0588	2.0089
s0022	100	2	>0.10	0.9363	>0.10	0.6376	>0.10	0.8219	>0.10	1.4664
s0039	100	1	>0.10	1.1066	0.0625	1.1982	0.0551	1.2810	>0.10	1.0798
s0040	200	3	0.0389	1.7357	>0.10	1.2649	0.0983	2.2353	0.0449	2.0825
s0059	300	3	0.0469	1.9686	0.0468	3.7769	0.0099	5.4146	>0.10	1.3547
s0063	300	2	0.0037	1.7351	0.0418	1.6450	>0.10	1.5656	>0.10	1.5060
s0068	700	2	0.0218	0.6445	>0.10	0.8501	>0.10	0.7793	0.0982	0.5632
s0072	6500	2	0.0627	1.4824	0.0069	2.2083	>0.10	1.0843	>0.10	0.7685
s0073P2	450	2	0.0023	0.5703	>0.10	0.7329	>0.10	0.6297	0.0987	0.4909
s0076x1	200	2	0.0807	1.2392	>0.10	0.6988	>0.10	0.9070	>0.10	1.1187
s0079I	400	2	0.0007	1.9503	0.0002	2.5357	>0.10	1.3644	>0.10	1.1705
s0081	60	2	0.0026	0.5093	0.0384	0.5774	>0.10	0.8913	>0.10	0.5235
s0137	2500	2	0.0322	1.4856	0.0745	1.5241	0.0872	1.8527	>0.10	1.2568
s0143P3	630	1	0.0932	1.0806	0.0342	1.1450	>0.10	1.1183	>0.10	1.0291
s0143P3	630	3	0.0294	1.7362	0.0103	2.1681	>0.10	1.7919	>0.10	1.2595
s0235	4500	2	0.0174	1.6960	0.0284	1.8866	>0.10	1.4827	>0.10	1.4227
s0237	1000	3	>0.10	1.3805	>0.10	1.9314	0.0431	3.2504	>0.10	0.9726
s0255n	1000	2	>0.10	0.7361	0.0933	0.6593	>0.10	0.6550	>0.10	0.9813
s0260	5400	2	>0.10	1.0896	0.0695	0.2945	>0.10	0.6016	>0.10	1.2113
s0296P1	225	2	0.0038	1.7491	0.0002	2.5560	0.0466	2.3419	>0.10	0.8519
s0303	300	2	0.0860	1.4072	>0.10	1.1960	>0.10	1.5662	>0.10	1.3788
s0305	8332	2	0.0809	1.2267	>0.10	1.1590	>0.10	0.9719	>0.10	1.2343
s0330x1	600	2	>0.10	0.9730	0.0134	3.3569	0.0632	5.4988	0.0555	0.0021
s0343	125	2	>0.10	0.7487	0.0795	0.6256	>0.10	0.5594	>0.10	1.1414
s0398	200	2	0.0125	0.4725	>0.10	0.6070	>0.10	0.8846	0.0725	0.1956
s0398	200	3	0.0551	0.3428	0.0790	0.3049	>0.10	0.4646	>0.10	0.6364
s0404	150	1	0.0321	1.1427	>0.10	1.1160	>0.10	1.1811	>0.10	1.0783
s0404	150	3	0.0087	1.8696	>0.10	1.7755	0.0727	2.3524	>0.10	1.4714
s0459	2700	2	>0.10	1.3287	>0.10	1.4538	>0.10	1.2304	>0.10	0.9768
s0545	900	2	0.0000	2.2547	0.0048	2.1037	>0.10	1.7913	0.0300	2.0266
s0654	400	3	0.0050	2.8738	>0.10	1.5890	>0.10	1.2356	0.0119	3.1822
s0670	900	2	>0.10	0.7709	0.0715	0.5411	0.0652	0.2800	>0.10	0.9506
s0676	1200	1	0.0088	1.1968	>0.10	1.0888	>0.10	1.2110	0.0130	1.2678
s0677	500	2	0.0041	1.7183	0.0289	1.7290	>0.10	1.1095	>0.10	1.3276
s0691NM	1575	2	0.0280	1.8399	>0.10	1.0211	>0.10	1.6936	0.0761	1.8725
s0702	178200	2	0.0005	1.9066	0.0000	2.8624	0.0120	2.6656	>0.10	0.9739
s6001	na	1	0.0292	0.8715	na	na	na	na	na	na
s6002	na	1	0.0027	0.8341	0.0214	0.8319	>0.10	0.8850	>0.10	0.9325
s6003	na	3	0.0176	1.9477	0.0051	3.1766	>0.10	1.3355	>0.10	1.2017
s6006	na	2	0.0194	1.5374	0.0958	1.5021	0.0135	2.3697	>0.10	1.2597
s6007	na	1	0.0756	1.1144	0.0107	1.2055	>0.10	1.0747	0.0342	0.9164

APPENDIX D

LUNG PROGNOSIS (HH COHORT)			All Log rank		Chi	Adenocarcinoma Log rank		Chi	Squamous cell Log rank		Chi
AGI ID	Dilution (1:X)	Scoring method	P value	Hazard ratio	square P value	P value	Hazard ratio	square P value	P value	Hazard ratio	square P value
s0021	1500	3	0.1288	1.8320	0.0240	0.2188	1.6167	0.0860	0.0005	0.0657	0.0100
s0022	250	2	0.0116	0.3747	0.1000	>0.10	nd	>0.10	>0.10	nd	>0.10
s0039	400	2	0.3532	1.5469	0.0080	>0.10	nd	>0.10	>0.10	nd	>0.10
s0046	300	2	0.0145	0.5165	0.0270	>0.10	nd	>0.10	0.0529	0.3302	0.0850
s0063	1200	2	>0.10	nd	>0.10	0.0831	1.8631	0.0550	>0.10	nd	>0.10
s0072	6500	2	0.2633	1.3570	0.0680	>0.10	nd	>0.10	>0.10	nd	>0.10
s0073P2	50	2	0.0935	0.4640	0.0430	>0.10	nd	>0.10	>0.10	nd	>0.10
s0074P3	810	3	0.0723	0.0022	0.0530	>0.10	nd	>0.10	>0.10	nd	>0.10
s0137	5000	2	0.0610	1.6429	0.1010	0.2271	1.5312	0.0660	>0.10	nd	>0.10
s0143P3	300	3	>0.10	nd	>0.10	0.0008	4.5211	0.0270	>0.10	nd	>0.10
s0296P1	1350	2	0.0783	1.6148	0.0460	0.0237	2.1849	0.0180	0.1042	0.3968	0.0840
s0303	300	2	>0.10	nd	>0.10	0.0469	2.0494	0.5360	>0.10	nd	>0.10
s0330	15000	3	>0.10	nd	>0.10	>0.10	nd	>0.10	0.0124	0.2278	0.0460
s0330	45000	3	0.0880	0.5248	0.0440	>0.10	nd	>0.10	0.0188	0.1270	0.0130
s0330x1	600	3	>0.10	nd	>0.10	>0.10	nd	>0.10	0.0455	0.1631	0.0080
s0331	300	3	0.2157	0.6603	0.0850	>0.10	nd	>0.10	0.0404	0.2350	0.0050
s0331x1	300	3	>0.10	nd	>0.10	>0.10	nd	>0.10	0.0705	0.2744	0.0360
s0332	400	3	0.1496	0.5639	0.0680	>0.10	nd	>0.10	0.0621	0.1785	0.0160
s0332x1	150	2	>0.10	nd	>0.10	>0.10	nd	>0.10	0.0321	0.1466	0.1290

APPENDIX D-continued

LUNG PROGNOSIS (HH COHORT)			All			Adenocarcinoma			Squamous cell		
			Log rank		Chi	Log rank		Chi	Log rank		Chi
AGI ID	Dilution (1:X)	Scoring method	P value	Hazard ratio	square P value	P value	Hazard ratio	square P value	P value	Hazard ratio	square P value
s0398	200	2	0.1253	0.5775	0.0870	>0.10	nd	>0.10	0.3348	0.6094	0.0640
s0404	900	3	0.1273	1.7817	0.0420	>0.10	nd	>0.10	>0.10	nd	>0.10
s0545	2700	2	0.1246	1.8432	0.0150	0.0191	3.2839	0.0180	>0.10	nd	>0.10
s0586	400	2	0.0204	0.4659	0.4380	0.1322	0.2457	0.0960	>0.10	nd	>0.10
s0691	1575	3	>0.10	nd	>0.10	>0.10	nd	>0.10	0.0608	3.1820	0.0420
s0702	178200	1	>0.10	nd	>0.10	>0.10	nd	>0.10	0.0463	0.6944	0.5360
s6006	1	2	>0.10	nd	>0.10	0.1259	1.7720	0.0550	>0.10	nd	>0.10
s6007	1	2	>0.10	nd	>0.10	0.0316	3.4266	0.0110	>0.10	nd	>0.10
s6008	1	2	>0.10	nd	>0.10	>0.10	nd	>0.10	0.2388	1312.0118	0.0230
s6013	1	2	>0.10	nd	>0.10	0.0154	2.5755	0.0540	>0.10	nd	>0.10
s0614	3000	2	0.0930	1.5785	0.0860	>0.10	nd	>0.10	>0.10	nd	>0.10

APPENDIX E

BREAST PROGNOSIS (HH COHORT)			All Log rank		ER Pos Log rank		ER Pos/ Node Neg Log rank		ER neg Log rank	
AGI ID	Dilution (1:X)	Scoring method	P value	Hazard ratio	P value	Hazard ratio	P value	Hazard ratio	P value	Hazard ratio
s0022	100	2	>0.10	0.8660	0.0633	0.5679	>0.10	0.8810	>0.10	1.3696
s0053	30	2	0.0496	0.6276	>0.10	0.7265	>0.10	1.0372	>0.10	0.5002
s0059P2	90	2	0.0088	1.9934	>0.10	1.7964	>0.10	1.8087	>0.10	1.4654
s0063	300	2	0.0031	1.7208	0.0955	1.5202	>0.10	1.5656	>0.10	1.7249
s0063	600	2	0.0006	1.9517	0.0154	2.0148	0.0660	2.4507	>0.10	1.4408
s0068	700	2	0.0312	0.6537	>0.10	0.8644	>0.10	0.7793	0.0936	0.5597
s0072	6500	2	>0.10	1.4087	0.0307	2.0193	>0.10	1.3344	>0.10	0.7426
s0073p2	450	2	0.0060	0.6051	>0.10	0.8755	>0.10	1.0495	>0.10	0.4614
s0076x1	200	2	0.0471	1.6431	>0.10	0.5060	>0.10	0.8227	>0.10	1.3384
s0079	400	2	0.0006	1.8382	0.0050	2.0469	>0.10	1.0820	>0.10	1.2420
s0081	60	2	0.0006	0.5518	0.0621	0.6335	>0.10	0.7897	>0.10	0.4758
s0140	500	2	0.0146	1.7628	>0.10	1.7553	>0.10	0.6881	>0.10	1.3817
s0235	4500	2	0.0002	1.9769	0.0017	2.1999	>0.10	1.5655	>0.10	1.5469
s0253	2000	2	0.0579	1.5740	>0.10	1.5128	0.0784	2.1386	>0.10	1.4763
s0253	500	2	>0.10	1.1127	>0.10	0.7030	>0.10	0.8017	0.0377	2.1389
s0255	1000	2	0.0610	0.6995	0.0603	0.6193	>0.10	0.6550	>0.10	0.8992
s0296P1	225	1	0.0028	1.1896	0.0001	1.3344	0.0008	1.3554	>0.10	0.9879
s0296P1	225	2	0.0052	1.7183	0.0014	2.3378	0.0466	2.3419	>0.10	0.8994
s0305	8332	2	0.0945	1.5035	>0.10	1.2945	>0.10	0.9447	>0.10	1.4199
s0330x1	600	2	>0.10	0.7456	0.0945	2.6186	0.0632	5.4988	0.0525	0.0021
s0404	150	2	0.0265	1.6475	>0.10	1.3534	>0.10	1.8109	>0.10	1.4264
s0404	150	3	0.0027	2.0719	0.0706	1.8942	0.0623	2.4347	>0.10	1.6912
s0440	1200	2	0.0581	0.6270	>0.10	0.8110	>0.10	0.6788	>0.10	0.2904
s0545	2700	2	0.0000	2.4278	>0.10	1.7002	>0.10	0.7788	0.0024	2.4284
s0545	900	2	0.0000	2.2447	0.0055	2.1160	>0.10	1.7913	0.0412	1.9465
s0654	400	2	>0.10	0.8150	0.0676	0.4627	>0.10	0.6037	>0.10	1.7718
s0670	900	2	>0.10	0.7040	0.0258	0.4379	0.0652	0.2800	>0.10	0.8549
s0676	1200	1	0.0113	1.1614	>0.10	1.0623	>0.10	1.2110	0.0212	1.2442
s0676	1200	2	0.0392	1.5231	>0.10	1.2602	>0.10	1.9314	0.0875	1.8335
s0677	1000	1	0.0017	1.1649	0.0076	1.2173	>0.10	1.0408	>0.10	1.0892
s0677	1000	2	0.0123	1.5683	0.0148	1.8170	>0.10	1.0567	>0.10	1.2487
s0687	1260	2	0.0830	0.6973	0.0519	0.5427	>0.10	1.1017	>0.10	0.8919
s0691	1575	1	0.0001	1.2824	>0.10	1.0463	>0.10	1.1225	0.0058	1.2902
s0691	1575	2	0.0020	2.1106	>0.10	1.1418	>0.10	1.6936	0.0217	2.1925
s0695	2700	2	0.0459	1.4465	>0.10	1.0295	>0.10	0.9663	>0.10	1.2102
s0702	178200	2	0.0001	2.0291	0.0000	3.1207	0.0010	3.3919	>0.10	1.0431
s6001	na	2	0.0009	0.5721	>0.10	1.0000	>0.10	1.0000	>0.10	1.0000
s6002	na	2	0.0004	0.5236	0.0083	0.5255	>0.10	0.6236	>0.10	0.9192
s6006	na	1	0.0413	1.1246	0.0591	1.1129	0.0334	1.3081	>0.10	1.0566
s6006	na	2	0.0399	1.4388	>0.10	1.3185	0.0095	2.4996	>0.10	1.2815
s6007	na	1	>0.10	1.1140	0.0086	1.1848	>0.10	1.0585	0.0284	0.9403
s6007	na	2	0.0358	1.4803	0.0537	1.6016	>0.10	1.0875	>0.10	0.9724
s6007	na	3	>0.10	1.1979	0.0032	2.4860	>0.10	2.1836	0.0232	0.4636

APPENDIX F

LUNG PROGNOSIS (HH & UAB COHORTS)			HH 5 yr recurrence		UAB 5 yr survival		
AGI ID	Dilution (1:X)	Scoring method	P value	Hazard ratio	P value	Hazard ratio	
s0073P2	50	2	0.129	0.497	0.192	0.660	All
s0074P3	810	3	0.091	0.002	0.096	0.002	
s0586	400	2	0.007	0.385	0.148	0.619	
s6007	1	2	0.081	2.420	0.112	2.099	
s0074P3	810	3	0.166	0.002	0.076	0.002	Adenocarcinoma
s0143P3	300	3	0.001	4.521	0.023	4.450	
s0296P1	1350	2	0.024	2.185	0.021	2.214	
s0303	300	2	0.047	2.049	0.007	3.358	
s6006	1	2	0.126	1.772	0.164	1.650	
s6007	1	2	0.032	3.427	0.033	2.734	

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 327

<210> SEQ ID NO 1
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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from VAV-3 protein

<400> SEQUENCE: 1

Asp Tyr Ile Ser Lys Ser Lys Glu Asp Val Lys Leu Lys
1 5 10

<210> SEQ ID NO 2
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from VAV-3 protein

<400> SEQUENCE: 2

Glu Lys Arg Thr Asn Gly Leu Arg Arg Thr Pro Lys Gln Val Asp
1 5 10 15

<210> SEQ ID NO 3
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from VAV-3 protein

<400> SEQUENCE: 3

Thr Glu Glu Ser Ile Asn Asp Glu Asp Ile Tyr Lys Gly Leu Pro Asp
1 5 10 15

Leu Ile Asp Glu
20

<210> SEQ ID NO 4
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from mammoglobin

<400> SEQUENCE: 4

Ser Lys Thr Ile Asn Pro Gln Val Ser Lys Thr Glu Tyr Lys Glu Leu
1 5 10 15

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Leu Gln Glu

<210> SEQ ID NO 5
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from mammoglobin

<400> SEQUENCE: 5

Asp Asp Asn Ala Thr Thr Asn Ala Ile Asp Glu Leu Lys Glu Cys
1 5 10 15

<210> SEQ ID NO 6
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from mammoglobin

<400> SEQUENCE: 6

Asn Gln Thr Asp Glu Thr Leu Ser Asn Val Glu Val Phe Met Gln
1 5 10 15

<210> SEQ ID NO 7
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from RB18A (P53 binding)

<400> SEQUENCE: 7

Ser Ser Asp Asp Gly Ile Arg Pro Leu Pro Glu Tyr Ser Thr Glu Lys
1 5 10 15

His Lys Lys

<210> SEQ ID NO 8
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from RB18A (P53 binding)

<400> SEQUENCE: 8

Asn Lys Thr Lys Lys Lys Lys Ser Ser Arg Leu Pro Pro Glu Lys
1 5 10 15

<210> SEQ ID NO 9
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from RB18A (P53 binding)

<400> SEQUENCE: 9

Asp Gly Lys Ser Lys Asp Lys Pro Pro Lys Arg Lys Lys Ala Asp Thr
1 5 10 15

Glu

<210> SEQ ID NO 10
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Putative cadherin-like protein

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<400> SEQUENCE: 10

Lys Asn Lys Glu Pro Leu Thr Lys Lys Gly Glu Thr Lys Thr Ala Glu
1 5 10 15

Arg Asp

<210> SEQ ID NO 11
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Putative cadherin-like protein

<400> SEQUENCE: 11

Lys Leu Thr Cys Thr Asp Leu Asp Ser Ser Pro Arg Ser Phe Arg Tyr
1 5 10 15

Ser

<210> SEQ ID NO 12
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Putative cadherin-like protein

<400> SEQUENCE: 12

Glu Val Asp Tyr Glu Asn Pro Ser Asn Leu Ala Ala Gly Asn Lys Tyr
1 5 10 15

Thr

<210> SEQ ID NO 13
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Sim to Cyto p450

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Lys Thr Leu Gln Val Phe Asn Pro Leu Arg Phe Ser Arg Glu Asn Ser
1 5 10 15

Glu Lys Ile His
20

<210> SEQ ID NO 14
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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Sim to Cyto p450

<400> SEQUENCE: 14

Gln His Phe Ala Ile Ile Glu Cys Lys Val Ala Val Ala Leu Thr
1 5 10 15

<210> SEQ ID NO 15
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Sim to Cyto p450

<400> SEQUENCE: 15

Arg Lys Phe Leu Ala Pro Asp His Ser Arg Pro Pro Gln Pro Val Arg
1 5 10 15

Gln

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<210> SEQ ID NO 16
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Chuck Ras

<400> SEQUENCE: 16

Val Leu Pro Leu Lys Asn Ile Leu Asp Glu Ile Lys Lys Pro Lys Asn
1 5 10 15

<210> SEQ ID NO 17
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Chuck Ras

<400> SEQUENCE: 17

Tyr Glu Leu Cys Arg Glu Val Arg Arg Arg Arg Met Val Gln Gly Lys
1 5 10 15

Thr

<210> SEQ ID NO 18
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Chuck Ras

<400> SEQUENCE: 18

Met Ala Lys Ser Ala Glu Val Lys Leu Ala Ile Phe Gly Arg Ala Gly
1 5 10 15

Val Gly Lys

<210> SEQ ID NO 19
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from MDGI

<400> SEQUENCE: 19

Lys Asn Thr Glu Ile Ser Phe Lys Leu Gly Val Glu Phe Asp Glu
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<210> SEQ ID NO 20
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from MDGI

<400> SEQUENCE: 20

His Leu Gln Lys Trp Asp Gly Gln Glu Thr Thr Leu Val Arg Glu
1 5 10 15

<210> SEQ ID NO 21
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from MDGI

<400> SEQUENCE: 21

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Thr Lys Pro Thr Thr Ile Ile Glu Lys Asn Gly Asp Ile Leu Thr Leu
1 5 10 15

Lys Thr His

<210> SEQ ID NO 22
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Human GABA-A receptor pi subunit

<400> SEQUENCE: 22

Leu Gln Gln Met Ala Ala Lys Asp Arg Gly Thr Thr Lys Glu Val Glu
1 5 10 15

Glu Val Ser

<210> SEQ ID NO 23
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Human GABA-A receptor pi subunit

<400> SEQUENCE: 23

Lys Arg Lys Ile Ser Phe Ala Ser Ile Glu Ile Ser Ser Asp Asn Val
1 5 10 15

Asp Tyr Ser Asp
20

<210> SEQ ID NO 24
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Human GABA-A receptor pi subunit

<400> SEQUENCE: 24

Asp Gly Asn Asp Val Glu Phe Thr Trp Leu Arg Gly Asn Asp Ser Val
1 5 10 15

Arg Gly Leu Glu His
20

<210> SEQ ID NO 25
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Annexin VIII

<400> SEQUENCE: 25

Gln Arg Gln Gln Ile Ala Lys Ser Phe Lys Ala Gln Phe Gly Lys Asp
1 5 10 15

Leu Thr Glu

<210> SEQ ID NO 26
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Annexin VIII

<400> SEQUENCE: 26

Arg Glu Ile Met Lys Ala Tyr Glu Glu Asp Tyr Gly Ser Ser Leu Glu
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-continued

Glu Asp Ile Gln
20

<210> SEQ ID NO 27
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Annexin VIII

<400> SEQUENCE: 27

Glu Glu Tyr Glu Lys Ile Ala Asn Lys Ser Ile Glu Asp Ser Ile Lys
1 5 10 15

Ser Glu

<210> SEQ ID NO 28
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from hypothetical UBCc containing protein

<400> SEQUENCE: 28

Glu Gly Gly Ser Leu Val Pro Ala Ala Arg Gln Gln His Cys Thr Gln
1 5 10 15

Val Arg Ser Arg Arg
20

<210> SEQ ID NO 29
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from hypothetical UBCc containing protein

<400> SEQUENCE: 29

Arg Lys Ala Gly Lys Ser Lys Lys Ser Phe Ser Arg Lys Glu Ala Glu
1 5 10 15

<210> SEQ ID NO 30
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from hypothetical UBCc containing protein

<400> SEQUENCE: 30

Lys Thr His Glu Lys Tyr Gly Trp Val Thr Pro Pro Val Ser Asp Gly
1 5 10 15

<210> SEQ ID NO 31
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from MDR1

<400> SEQUENCE: 31

Met Asp Leu Glu Gly Asp Arg Asn Gly Gly Ala Lys Lys Lys Asn
1 5 10 15

<210> SEQ ID NO 32
<211> LENGTH: 19
<212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from MDR1

<400> SEQUENCE: 32

Asn Leu Glu Asp Leu Met Ser Asn Ile Thr Asn Arg Ser Asp Ile Asn
1 5 10 15

Asp Thr Gly

<210> SEQ ID NO 33
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from MDR1

<400> SEQUENCE: 33

Arg Gly Ser Gln Ala Gln Asp Arg Lys Leu Ser Thr Lys Glu Ala
1 5 10 15

<210> SEQ ID NO 34
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from MDR3

<400> SEQUENCE: 34

Met Asp Leu Glu Ala Ala Lys Asn Gly Thr Ala Trp Arg Pro Thr Ser
1 5 10 15

Ala Glu

<210> SEQ ID NO 35
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from MDR3

<400> SEQUENCE: 35

Asn Phe Ser Phe Pro Val Asn Phe Ser Leu Ser Leu Leu Asn Pro Gly
1 5 10 15

Lys

<210> SEQ ID NO 36
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from MDR3

<400> SEQUENCE: 36

Lys Asn Ser Gln Met Cys Gln Lys Ser Leu Asp Val Glu Thr Asp Gly
1 5 10 15

<210> SEQ ID NO 37
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from MRP-1

<400> SEQUENCE: 37

Met Ala Leu Arg Gly Phe Cys Ser Ala Asp Gly Ser Asp
1 5 10

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<210> SEQ ID NO 38
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from MRP-1

<400> SEQUENCE: 38

Lys Asn Trp Lys Lys Glu Cys Ala Lys Thr Arg Lys Gln Pro Val Lys
1 5 10 15

<210> SEQ ID NO 39
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from MRP-1

<400> SEQUENCE: 39

Asp Ser Ile Glu Arg Arg Pro Val Lys Asp Gly Gly Gly Thr Asn Ser
1 5 10 15

<210> SEQ ID NO 40
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from MRP2/CMOAT

<400> SEQUENCE: 40

Met Leu Glu Lys Phe Cys Asn Ser Thr Phe Trp Asn Ser Ser Phe Leu
1 5 10 15

Asp Ser Pro Glu
20

<210> SEQ ID NO 41
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from MRP2/CMOAT

<400> SEQUENCE: 41

Ser Ile Leu Cys Gly Thr Phe Gln Phe Gln Thr Leu Ile Arg Thr
1 5 10 15

<210> SEQ ID NO 42
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from MRP2/CMOAT

<400> SEQUENCE: 42

Glu Asn Asn Glu Ser Ser Asn Asn Pro Ser Ser Ile Ala Ser
1 5 10

<210> SEQ ID NO 43
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from MRP4

<400> SEQUENCE: 43

Gln Glu Val Lys Pro Asn Pro Leu Gln Asp Ala Asn Ile Cys Ser Arg
1 5 10 15

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<210> SEQ ID NO 44
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from MRP4

<400> SEQUENCE: 44

Asp Glu Ile Ser Gln Arg Asn Arg Gln Leu Pro Ser Asp Gly Lys Lys
1 5 10 15

<210> SEQ ID NO 45
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from MRP4

<400> SEQUENCE: 45

Val Gln Asp Phe Thr Ala Phe Trp Asp Lys Ala Ser Glu Thr Pro Thr
1 5 10 15

Leu Gln

<210> SEQ ID NO 46
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from MRP3/ CMOAT2

<400> SEQUENCE: 46

Met Asp Ala Leu Cys Gly Ser Gly Glu Leu Gly Ser Lys Phe Trp Asp
1 5 10 15

Ser Asn

<210> SEQ ID NO 47
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from MRP3/ CMOAT2

<400> SEQUENCE: 47

Arg Lys Gln Glu Lys Gln Thr Ala Arg His Lys Ala Ser Ala Ala
1 5 10 15

<210> SEQ ID NO 48
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from MRP3/ CMOAT2

<400> SEQUENCE: 48

Asp Pro Gln Ser Val Glu Arg Lys Thr Ile Ser Pro Gly
1 5 10

<210> SEQ ID NO 49
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from MRP5/ MOAT-C

<400> SEQUENCE: 49

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Met Lys Asp Ile Asp Ile Gly Lys Glu Tyr Ile Ile Pro Ser Pro Gly
1 5 10 15

Tyr Arg Ser

<210> SEQ ID NO 50
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from MRP5/ MOAT-C

<400> SEQUENCE: 50

Arg Asp Arg Glu Asp Ser Lys Phe Arg Arg Thr Arg Pro Leu Glu Cys
1 5 10 15

Gln Asp

<210> SEQ ID NO 51
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from MRP5/ MOAT-C

<400> SEQUENCE: 51

Ser Lys His Glu Ser Ser Asp Val Asn Cys Arg Arg Leu Glu Arg
1 5 10 15

<210> SEQ ID NO 52
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from MRP6

<400> SEQUENCE: 52

Met Ala Ala Pro Ala Glu Pro Cys Ala Gly Gln Gly Val Trp Asn Gln
1 5 10 15

Thr Glu Pro Glu
20

<210> SEQ ID NO 53
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from MRP6

<400> SEQUENCE: 53

Asp Pro Gly Val Val Asp Ser Ser Ser Ser Gly Ser Ala Ala Gly Lys
1 5 10 15

Asp

<210> SEQ ID NO 54
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from MRP6

<400> SEQUENCE: 54

His Thr Leu Val Ala Glu Asn Ala Met Asn Ala Glu Lys
1 5 10

<210> SEQ ID NO 55
<211> LENGTH: 15

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from BSEP

<400> SEQUENCE: 55

Gln Glu Val Leu Ser Lys Ile Gln His Gly His Thr Ile Ile Ser
1 5 10 15

<210> SEQ ID NO 56
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from BSEP

<400> SEQUENCE: 56

Thr Asn Ser Ser Leu Asn Gln Asn Met Thr Asn Gly Thr Arg
1 5 10

<210> SEQ ID NO 57
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from BSEP

<400> SEQUENCE: 57

Met Ser Asp Ser Val Ile Leu Arg Ser Ile Lys Lys Phe Gly Glu Glu
1 5 10 15

Asn Asp

<210> SEQ ID NO 58
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from ATP-binding cassette, sub-family B, member 10

<400> SEQUENCE: 58

Gly Ala Asp Asp Pro Ser Ser Val Thr Ala Glu Glu Ile Gln Arg
1 5 10 15

<210> SEQ ID NO 59
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from ATP-binding cassette, sub-family B, member 10

<400> SEQUENCE: 59

Asn Ala Val Ala Ser Pro Glu Phe Pro Pro Arg Phe Asn Thr
1 5 10

<210> SEQ ID NO 60
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from ATP-binding cassette, sub-family B, member 10

<400> SEQUENCE: 60

Lys Pro Asn Gly Ile Tyr Arg Lys Leu Met Asn Lys Gln Ser Phe Ile
1 5 10 15

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Ser Ala

<210> SEQ ID NO 61
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from TAP1

<400> SEQUENCE: 61

Met Ala Ser Ser Arg Cys Pro Ala Pro Arg Gly Cys Arg
1 5 10

<210> SEQ ID NO 62
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from TAP1

<400> SEQUENCE: 62

Gln Gly Gly Ser Gly Asn Pro Val Arg Arg
1 5 10

<210> SEQ ID NO 63
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from TAP1

<400> SEQUENCE: 63

Glu Phe Val Gly Asp Gly Ile Tyr Asn Asn Thr Met Gly His Val His
1 5 10 15

Ser

<210> SEQ ID NO 64
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from SUR1

<400> SEQUENCE: 64

Met Pro Leu Ala Phe Cys Gly Ser Glu Asn His Ser Ala Ala Tyr Arg
1 5 10 15

<210> SEQ ID NO 65
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from SUR1

<400> SEQUENCE: 65

Asp His Leu Gly Lys Glu Asn Asp Val Phe Gln Pro Lys Thr Gln Phe
1 5 10 15

Leu Gly

<210> SEQ ID NO 66
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from SUR1

<400> SEQUENCE: 66

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Glu Ile Arg Glu Glu Gln Cys Ala Pro His Glu Pro Thr Pro Gln Gly
1 5 10 15

<210> SEQ ID NO 67
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from SUR2

<400> SEQUENCE: 67

Met Ser Leu Ser Phe Cys Gly Asn Asn Ile Ser Ser
1 5 10

<210> SEQ ID NO 68
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from SUR2

<400> SEQUENCE: 68

Gln Arg Val Asn Glu Thr Gln Asn Gly Thr Asn Asn Thr Thr Gly Ile
1 5 10 15

Ser Glu

<210> SEQ ID NO 69
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from SUR2

<400> SEQUENCE: 69

Asp Glu Ile Gly Asp Asp Ser Trp Arg Thr Gly Glu Ser Ser Leu Pro
1 5 10 15

Phe Glu Ser

<210> SEQ ID NO 70
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from INTEGRAL MEMBRANE PROTEIN 2B

<400> SEQUENCE: 70

Met Val Lys Val Thr Phe Asn Ser Ala Leu Ala Gln Lys Glu Ala Lys
1 5 10 15

Lys Asp Glu Pro Lys
20

<210> SEQ ID NO 71
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from INTEGRAL MEMBRANE PROTEIN 2B

<400> SEQUENCE: 71

Gln Thr Ile Glu Glu Asn Ile Lys Ile Phe Glu Glu Glu Glu Val Glu
1 5 10 15

<210> SEQ ID NO 72
<211> LENGTH: 21
<212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from INTEGRAL MEMBRANE PROTEIN 2B

<400> SEQUENCE: 72

His Asp Lys Glu Thr Tyr Lys Leu Gln Arg Arg Glu Thr Ile Lys Gly
1 5 10 15

Ile Gln Lys Arg Glu
20

<210> SEQ ID NO 73
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from ANK-3

<400> SEQUENCE: 73

His Lys Lys Glu Thr Glu Ser Asp Gln Asp Asp Glu Ile Glu Lys Thr
1 5 10 15

Asp Arg Arg Gln
20

<210> SEQ ID NO 74
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from ANK-3

<400> SEQUENCE: 74

Glu Gly Phe Lys Val Lys Thr Lys Lys Glu Ile Arg His Val Glu Lys
1 5 10 15

Lys Ser His Ser
20

<210> SEQ ID NO 75
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from ANK-3

<400> SEQUENCE: 75

Met Ala His Ala Ala Ser Gln Leu Lys Lys Asn Arg Asp Leu Glu Ile
1 5 10 15

Asn Ala Glu Glu
20

<210> SEQ ID NO 76
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from hypothetical protein FLJ21918

<400> SEQUENCE: 76

Glu Arg Ala Leu Ala Ala Ala Gln Arg Cys His Lys Lys Val Met Lys
1 5 10 15

Glu Arg

<210> SEQ ID NO 77
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Peptide from hypothetical protein FLJ21918

<400> SEQUENCE: 77

Thr Ala Gly Met Lys Asp Leu Leu Ser Val Phe Gln Ala Tyr Gln
1 5 10 15

<210> SEQ ID NO 78
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from hypothetical protein FLJ21918

<400> SEQUENCE: 78

Asp Pro Pro Arg Thr Val Leu Gln Ala Pro Lys Glu Trp Val Cys Leu
1 5 10 15

<210> SEQ ID NO 79
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from ataxia-telangiectasia group D-associated protein

<400> SEQUENCE: 79

Met Glu Ala Ala Asp Ala Ser Arg Ser Asn Gly Ser Ser Pro Glu Ala
1 5 10 15

Arg Asp Ala Arg
20

<210> SEQ ID NO 80
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from ataxia-telangiectasia group D-associated protein

<400> SEQUENCE: 80

Glu Leu His Leu Lys Pro His Leu Glu Gly Ala Ala Phe Arg Asp His
1 5 10 15

Gln

<210> SEQ ID NO 81
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from ataxia-telangiectasia group D-associated protein

<400> SEQUENCE: 81

Glu Gly Glu Gly Leu Gly Gln Ser Leu Gly Asn Phe Lys Asp Asp Leu
1 5 10 15

Leu Asn

<210> SEQ ID NO 82
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from ataxia-telangiectasia group D-associated protein

<400> SEQUENCE: 82

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Glu Leu His Leu Lys Pro His Leu Glu Gly Ala Ala Phe Arg Asp His
1 5 10 15

Gln

<210> SEQ ID NO 83
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from iroquois related homeobox 3

<400> SEQUENCE: 83

Gly Ser Glu Glu Arg Gly Ala Gly Arg Gly Ser Ser Gly Gly Arg Glu
1 5 10 15

Glu

<210> SEQ ID NO 84
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from iroquois related homeobox 3

<400> SEQUENCE: 84

Lys Ile Trp Ser Leu Ala Glu Thr Ala Thr Ser Pro Asp Asn Pro Arg
1 5 10 15

Arg Ser

<210> SEQ ID NO 85
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from iroquois related homeobox 3

<400> SEQUENCE: 85

Lys Lys Leu Leu Lys Thr Ala Phe Gln Pro Val Pro Arg Arg Pro Gln
1 5 10 15

Asn His Leu Asp
20

<210> SEQ ID NO 86
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Chuck Ras C-term

<400> SEQUENCE: 86

Arg Arg Ser Ser Thr Thr His Val Lys Gln Ala Ile Asn Lys Met Leu
1 5 10 15

Thr Lys Ile Ser Ser
20

<210> SEQ ID NO 87
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from putative G protein-coupled receptor (NP_055188.1|)

<400> SEQUENCE: 87

Met Arg Arg Lys Asn Thr Cys Gln Asn Phe Met Glu Tyr Phe Cys Ile

-continued

1 5 10 15

Ser Leu Ala Phe
20

<210> SEQ ID NO 88
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from putative G protein-coupled receptor (NP_055188.1|)

<400> SEQUENCE: 88

Asn Glu Thr Ile Leu Tyr Phe Pro Phe Ser Ser His Ser Ser Tyr Thr
1 5 10 15

Val Arg Ser Lys Lys
20

<210> SEQ ID NO 89
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from putative G protein-coupled receptor (NP_055188.1|)

<400> SEQUENCE: 89

Lys Val Gln Ile Pro Ala Tyr Ile Glu Met Asn Ile Pro Leu Val Ile
1 5 10 15

Leu Cys Gln

<210> SEQ ID NO 90
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Calgranulin A

<400> SEQUENCE: 90

Met Leu Thr Glu Leu Glu Lys Ala Leu Asn Ser Ile Ile Asp Val Tyr
1 5 10 15

His Lys

<210> SEQ ID NO 91
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Calgranulin A

<400> SEQUENCE: 91

Arg Asp Asp Leu Lys Lys Leu Leu Glu Thr Glu Cys Pro Gln Tyr Ile
1 5 10 15

Arg Lys Lys Gly Ala Asp
20

<210> SEQ ID NO 92
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Calgranulin A

<400> SEQUENCE: 92

Lys Met Gly Val Ala Ala His Lys Lys Ser His Glu Glu Ser His Lys

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1 5 10 15

Glu

<210> SEQ ID NO 93
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from hepatocyte nuclear protein 3, alpha

<400> SEQUENCE: 93

Pro Glu Ser Arg Lys Asp Pro Ser Gly Ala Ser Asn Pro Ser Ala Asp
1 5 10 15

Ser

<210> SEQ ID NO 94
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from hepatocyte nuclear protein 3, alpha

<400> SEQUENCE: 94

His Gly Leu Ala Pro His Glu Ser Gln Leu His Leu Lys Gly Asp
1 5 10 15

<210> SEQ ID NO 95
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from hepatocyte nuclear protein 3, alpha

<400> SEQUENCE: 95

Glu Gln Gln His Lys Leu Asp Phe Lys Ala Tyr Glu Gln Ala Leu Gln
1 5 10 15

Tyr Ser

<210> SEQ ID NO 96
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from hepatocyte nuclear protein 3, alpha

<400> SEQUENCE: 96

Pro Glu Ser Arg Lys Asp Pro Ser Gly Ala Ser Asn Pro Ser Ala Asp
1 5 10 15

Ser

<210> SEQ ID NO 97
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from hepatocyte nuclear protein 3, alpha

<400> SEQUENCE: 97

His Gly Leu Ala Pro His Glu Ser Gln Leu His Leu Lys Gly Asp
1 5 10 15

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<210> SEQ ID NO 98
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from hepatocyte nuclear protein 3, alpha

<400> SEQUENCE: 98

Glu Gln Gln His Lys Leu Asp Phe Lys Ala Tyr Glu Gln Ala Leu Gln
1 5 10 15

Tyr Ser

<210> SEQ ID NO 99
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from intestinal trefoil precursor

<400> SEQUENCE: 99

Glu Glu Tyr Val Gly Leu Ser Ala Asn Gln Cys Ala Val Pro Ala Lys
1 5 10 15

Asp Arg Val Asp
20

<210> SEQ ID NO 100
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from intestinal trefoil precursor

<400> SEQUENCE: 100

Arg Val Asp Cys Gly Tyr Pro His Val Thr Pro Lys Glu Cys Asn
1 5 10 15

<210> SEQ ID NO 101
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from intestinal trefoil precursor

<400> SEQUENCE: 101

Val Pro Trp Cys Phe Lys Pro Leu Gln Glu Ala Glu Cys Thr Phe
1 5 10 15

<210> SEQ ID NO 102
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from intestinal trefoil precursor

<400> SEQUENCE: 102

Val Pro Trp Cys Phe Lys Pro Leu Gln Glu Ala Glu Cys Thr Phe
1 5 10 15

<210> SEQ ID NO 103
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Keratin 17

<400> SEQUENCE: 103

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Lys Lys Glu Pro Val Thr Thr Arg Gln Val Arg Thr Ile Val Glu Glu
1 5 10 15

<210> SEQ ID NO 104
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Keratin 17

<400> SEQUENCE: 104

Gln Asp Gly Lys Val Ile Ser Ser Arg Glu Gln Val His Gln Thr Thr
1 5 10 15

Arg

<210> SEQ ID NO 105
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Keratin 17

<400> SEQUENCE: 105

Ser Ser Ser Ile Lys Gly Ser Ser Gly Leu Gly Gly Gly Ser Ser
1 5 10 15

<210> SEQ ID NO 106
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from LIV-1

<400> SEQUENCE: 106

Asp His Asn His Ala Ala Ser Gly Lys Asn Lys Arg Lys Ala Leu Cys
1 5 10 15

Pro Asp His Asp
20

<210> SEQ ID NO 107
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from LIV-1

<400> SEQUENCE: 107

Glu Glu Pro Ala Met Glu Met Lys Arg Gly Pro Leu Phe Ser His Leu
1 5 10 15

Ser Ser Gln Asn Ile
20

<210> SEQ ID NO 108
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from LIV-1

<400> SEQUENCE: 108

Gln Arg Tyr Ser Arg Glu Glu Leu Lys Asp Ala Gly Val Ala Thr Leu
1 5 10 15

<210> SEQ ID NO 109
<211> LENGTH: 22

-continued

<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from NAT1

<400> SEQUENCE: 109

Met Asp Ile Glu Ala Tyr Leu Glu Arg Ile Gly Tyr Lys Lys Ser Arg
1 5 10 15

Asn Lys Leu Asp Leu Glu
20

<210> SEQ ID NO 110
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from NAT1

<400> SEQUENCE: 110

Gln Met Trp Gln Pro Leu Glu Leu Ile Ser Gly Lys Asp Gln Pro Gln
1 5 10 15

Val Pro Cys Val Phe Arg
20

<210> SEQ ID NO 111
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from NAT1

<400> SEQUENCE: 111

Phe Asn Ile Ser Leu Gln Arg Lys Leu Val Pro Lys His Gly Asp Arg
1 5 10 15

Phe Phe Thr Ile
20

<210> SEQ ID NO 112
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from x-box binding

<400> SEQUENCE: 112

Gln Pro Pro Phe Leu Cys Gln Trp Gly Arg His Gln Pro Ser Trp Lys
1 5 10 15

Pro Leu Met Asn
20

<210> SEQ ID NO 113
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from x-box binding

<400> SEQUENCE: 113

Glu Lys Thr His Gly Leu Val Val Glu Asn Gln Glu Leu Arg Gln Arg
1 5 10 15

Leu Gly Met Asp
20

<210> SEQ ID NO 114
<211> LENGTH: 21

-continued

<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from x-box binding

<400> SEQUENCE: 114

Arg Gln Arg Leu Thr His Leu Ser Pro Glu Glu Lys Ala Leu Arg Arg
1 5 10 15

Lys Leu Lys Asn Arg
20

<210> SEQ ID NO 115
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from ATPase, H+ transporting, lysosomal (vacuolar proton pump), beta polypeptide, 56/58kD, isoform 1R7340

<400> SEQUENCE: 115

Arg Glu His Met Gln Ala Val Thr Arg Asn Tyr Ile Thr His Pro Arg
1 5 10 15

<210> SEQ ID NO 116
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from ATPase, H+ transporting, lysosomal (vacuolar proton pump), beta polypeptide, 56/58kD, isoform 1R7340

<400> SEQUENCE: 116

Lys Lys Ser Lys Ala Val Leu Asp Tyr His Asp Asp Asn
1 5 10

<210> SEQ ID NO 117
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from ATPase, H+ transporting, lysosomal (vacuolar proton pump), beta polypeptide, 56/58kD, isoform 1R7340

<400> SEQUENCE: 117

Asp Glu Phe Tyr Ser Arg Glu Gly Arg Leu Gln Asp Leu Ala Pro Asp
1 5 10 15

Thr Ala Leu

<210> SEQ ID NO 118
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from hypothetical protein MGC2714 (in part)

<400> SEQUENCE: 118

Arg Tyr Ala Phe Asp Phe Ala Arg Asp Lys Asp Gln Arg Ser Leu Asp
1 5 10 15

Ile Asp

<210> SEQ ID NO 119
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from hypothetical protein MGC2714 (in

-continued

part)

<400> SEQUENCE: 119

Ser Val Phe Tyr Gln Tyr Leu Glu Gln Ser Lys Tyr Arg Val Met Asn
1 5 10 15

Lys Asp Gln

<210> SEQ ID NO 120
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from hypothetical protein MGC2714 (in part)

<400> SEQUENCE: 120

Glu Asp Gly Ala Trp Pro Val Leu Leu Asp Glu Phe Val Glu Trp Gln
1 5 10 15

Lys Val Arg Gln Thr Ser
20

<210> SEQ ID NO 121
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Reproduction 8

<400> SEQUENCE: 121

Ser Phe Lys Ser Pro Gln Val Tyr Leu Lys Glu Glu Glu Glu Lys Asn
1 5 10 15

Glu Lys Arg

<210> SEQ ID NO 122
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Reproduction 8

<400> SEQUENCE: 122

Arg Lys Lys Gln Gln Glu Ala Gln Gly Glu Lys Ala Ser Arg Tyr Ile
1 5 10 15

Glu

<210> SEQ ID NO 123
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Reproduction 8

<400> SEQUENCE: 123

Glu Asp Ile Gly Ile Thr Val Asp Thr Val Leu Ile Leu Glu Glu Lys
1 5 10 15

Glu Gln Thr Asn
20

<210> SEQ ID NO 124
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from slit1

-continued

<400> SEQUENCE: 124

Asp Phe Arg Cys Glu Glu Gly Gln Glu Glu Gly Gly Cys Leu Pro Arg
1 5 10 15

Pro Gln

<210> SEQ ID NO 125
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from slit1

<400> SEQUENCE: 125

Asp Gly Thr Ser Phe Ala Glu Glu Val Glu Lys Pro Thr Lys Cys Gly
1 5 10 15

Cys Ala Leu Cys Ala
20

<210> SEQ ID NO 126
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from slit1

<400> SEQUENCE: 126

Lys Ala Phe Arg Gly Ala Thr Asp Leu Lys Asn Leu Arg Leu Asp Lys
1 5 10 15

Asn Gln

<210> SEQ ID NO 127
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from sry-box9

<400> SEQUENCE: 127

Met Asn Leu Leu Asp Pro Phe Met Lys Met Thr Asp Glu Gln Glu Lys
1 5 10 15

Gly Leu Ser

<210> SEQ ID NO 128
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from sry-box9

<400> SEQUENCE: 128

Asn Thr Phe Pro Lys Gly Glu Pro Asp Leu Lys Lys Glu Ser Glu Glu
1 5 10 15

Asp Lys

<210> SEQ ID NO 129
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from sry-box9

<400> SEQUENCE: 129

Lys Asn Gly Gln Ala Glu Ala Glu Glu Ala Thr Glu Gln Thr His Ile
1 5 10 15

-continued

Ser Pro Asn

<210> SEQ ID NO 130
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from EGF-Like Domain, Multiple 2

<400> SEQUENCE: 130

Gln Ala Ser Ser Leu Arg Leu Glu Pro Gly Arg Ala Asn Asp Gly Asp
1 5 10 15

Trp His

<210> SEQ ID NO 131
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from EGF-Like Domain, Multiple 2

<400> SEQUENCE: 131

Glu Leu Lys Gly Phe Ala Glu Arg Leu Gln Arg Asn Glu Ser Gly Leu
1 5 10 15

Asp Ser Gly Arg
20

<210> SEQ ID NO 132
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from EGF-Like Domain, Multiple 2

<400> SEQUENCE: 132

Arg Ser Gly Lys Ser Gln Pro Ser Tyr Ile Pro Phe Leu Leu Arg Glu
1 5 10 15

Glu

<210> SEQ ID NO 133
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Gamma-glytamyl hydrolase

<400> SEQUENCE: 133

Arg Arg Ser Asp Tyr Ala Lys Val Ala Lys Ile Phe Tyr Asn Leu Ser
1 5 10 15

Ile Gln Ser Phe Asp Asp
20

<210> SEQ ID NO 134
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Gamma-glytamyl hydrolase

<400> SEQUENCE: 134

Lys Asn Phe Thr Met Asn Glu Lys Leu Lys Lys Phe Phe Asn Val Leu
1 5 10 15

Thr Thr Asn

-continued

<210> SEQ ID NO 135
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Gamma-glytamyl hydrolase

<400> SEQUENCE: 135

Glu Phe Phe Val Asn Glu Ala Arg Lys Asn Asn His His Phe Lys Ser
1 5 10 15

Glu Ser Glu Glu
20

<210> SEQ ID NO 136
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Bullous Pemphigoid Antigen 1

<400> SEQUENCE: 136

Lys Asn Thr Gln Ala Ala Glu Ala Leu Val Lys Leu Tyr Glu Thr Lys
1 5 10 15

Leu Cys Glu

<210> SEQ ID NO 137
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Bullous Pemphigoid Antigen 1

<400> SEQUENCE: 137

Gln Glu Asn Gln Pro Glu Asn Ser Lys Thr Leu Ala Thr Gln Leu Asn
1 5 10 15

Gln

<210> SEQ ID NO 138
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Bullous Pemphigoid Antigen 1

<400> SEQUENCE: 138

Lys Gln Met Glu Lys Asp Leu Ala Phe Gln Lys Gln Val Ala Glu Lys
1 5 10 15

Gln Leu Lys

<210> SEQ ID NO 139
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from fasn

<400> SEQUENCE: 139

Glu Phe Val Glu Gln Leu Arg Lys Glu Gly Val Phe Ala Lys Glu Val
1 5 10 15

Arg

<210> SEQ ID NO 140
<211> LENGTH: 18
<212> TYPE: PRT

-continued

<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from fasn

<400> SEQUENCE: 140

Asp Arg His Pro Gln Ala Leu Glu Ala Ala Gln Ala Glu Leu Gln Gln
1 5 10 15

His Asp

<210> SEQ ID NO 141
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from fasn

<400> SEQUENCE: 141

Arg Glu Val Arg Gln Leu Thr Leu Arg Lys Leu Gln Glu Leu Ser Ser
1 5 10 15

Lys Ala Asp Glu
20

<210> SEQ ID NO 142
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Matrix Metalloproteinase 14

<400> SEQUENCE: 142

Ala Tyr Ile Arg Glu Gly His Glu Lys Gln Ala Asp Ile Met Ile Phe
1 5 10 15

Phe Ala Glu

<210> SEQ ID NO 143
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Matrix Metalloproteinase 14

<400> SEQUENCE: 143

Asp Glu Ala Ser Leu Glu Pro Gly Tyr Pro Lys His Ile Lys Glu Leu
1 5 10 15

Gly Arg

<210> SEQ ID NO 144
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Matrix Metalloproteinase 14

<400> SEQUENCE: 144

Arg Gly Ser Phe Met Gly Ser Asp Glu Val Phe Thr Tyr Phe Tyr Lys
1 5 10 15

<210> SEQ ID NO 145
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from ABP/ZF

<400> SEQUENCE: 145

-continued

Arg Gln Glu His Cys Met Ser Glu His Phe Lys Asn Arg Pro Ala Cys
1 5 10 15

Leu Gly Ala Arg
20

<210> SEQ ID NO 146
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from ABP/ZF

<400> SEQUENCE: 146

Gln Gly His Lys Trp Gly Glu Ser Pro Ser Gln Gly Thr Gln Ala Gly
1 5 10 15

Ala Gly Lys

<210> SEQ ID NO 147
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from ABP/ZF

<400> SEQUENCE: 147

Arg Ala Cys Gly Lys Arg Val Ser Glu Gly Asp Arg Asn Gly Ser Gly
1 5 10 15

Gly Gly Lys Trp Gly
20

<210> SEQ ID NO 148
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from fatty acid binding protein 7, FABP7

<400> SEQUENCE: 148

Met Val Glu Ala Phe Cys Ala Thr Trp Lys Leu Thr Asn Ser Gln Asn
1 5 10 15

<210> SEQ ID NO 149
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from fatty acid binding protein 7, FABP7

<400> SEQUENCE: 149

Gln Val Gly Asn Val Thr Lys Pro Thr Val Ile Ile Ser Gln Glu
1 5 10 15

<210> SEQ ID NO 150
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from fatty acid binding protein 7, FABP7

<400> SEQUENCE: 150

Lys Val Val Ile Arg Thr Leu Ser Thr Phe Lys Asn Thr Glu
1 5 10

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<210> SEQ ID NO 151
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Cadherin 3

<400> SEQUENCE: 151

Arg Ala Val Phe Arg Glu Ala Glu Val Thr Leu Glu Ala Gly Gly Ala
1 5 10 15

Glu Gln Glu

<210> SEQ ID NO 152
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Cadherin 3

<400> SEQUENCE: 152

Gln Glu Pro Ala Leu Phe Ser Thr Asp Asn Asp Asp Phe Thr Val Arg
1 5 10 15

Asn

<210> SEQ ID NO 153
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Cadherin 3

<400> SEQUENCE: 153

Gln Lys Tyr Glu Ala His Val Pro Glu Asn Ala Val Gly His Glu
1 5 10 15

<210> SEQ ID NO 154
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from GRO1 Oncogene

<400> SEQUENCE: 154

Lys Lys Ile Ile Glu Lys Met Leu Asn Ser Asp Lys Ser Asn
1 5 10

<210> SEQ ID NO 155
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Effector cell protease receptor 1

<400> SEQUENCE: 155

Gly Lys Pro Gly Asn Gln Asn Ser Lys Asn Glu Pro Pro Lys Lys Arg
1 5 10 15

Glu Arg Glu Arg
20

<210> SEQ ID NO 156
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Effector cell protease receptor 1

<400> SEQUENCE: 156

-continued

Gln Ala Glu Ala Pro Leu Val Pro Leu Ser Arg Gln Asn Lys
1 5 10

<210> SEQ ID NO 157
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Effector cell protease receptor 1

<400> SEQUENCE: 157

Asn Cys Phe Leu Thr Glu Arg Lys Ala Gln Pro Asp Glu
1 5 10

<210> SEQ ID NO 158
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from PLOD2

<400> SEQUENCE: 158

Lys Gln Val Asp Leu Glu Asn Val Trp Leu Asp Phe Ile Arg Glu
1 5 10 15

<210> SEQ ID NO 159
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from PLOD2

<400> SEQUENCE: 159

Glu Phe Asp Thr Val Asp Leu Ser Ala Val Asp Val His Pro Asn
1 5 10 15

<210> SEQ ID NO 160
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from PLOD2

<400> SEQUENCE: 160

Asn Lys Glu Val Tyr His Glu Lys Asp Ile Lys Val Phe Phe Asp Lys
1 5 10 15

Ala Lys

<210> SEQ ID NO 161
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Cytochrome p450, subfamily IIa

<400> SEQUENCE: 161

Lys Arg Gly Ile Glu Glu Arg Ile Gln Glu Glu Ser Gly Phe Leu Ile
1 5 10 15

Glu

<210> SEQ ID NO 162
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Cytochrome p450, subfamily IIa

-continued

<400> SEQUENCE: 162

Asp Arg Val Ile Gly Lys Asn Arg Gln Pro Lys Phe Glu Asp Arg Thr
1 5 10 15

Lys

<210> SEQ ID NO 163
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Cytochrome p450, subfamily IIa

<400> SEQUENCE: 163

Asn Pro Gln His Phe Leu Asp Asp Lys Gly Gln Phe Lys Lys Ser Asp
1 5 10 15

<210> SEQ ID NO 164
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Putative nucleoside
transporter-like protein

<400> SEQUENCE: 164

Arg His Cys Ile Leu Gly Glu Trp Leu Pro Ile Leu Ile Met Ala Val
1 5 10 15

Phe Asn

<210> SEQ ID NO 165
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Putative nucleoside
transporter-like protein

<400> SEQUENCE: 165

Lys Gln Arg Glu Leu Ala Gly Asn Thr Met Thr Val Ser Tyr Met Ser
1 5 10 15

<210> SEQ ID NO 166
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Putative nucleoside
transporter-like protein

<400> SEQUENCE: 166

Arg Asn Ala His Gly Ser Cys Leu His Ala Ser Thr Ala Asn Gly Ser
1 5 10 15

Ile Leu Ala Gly Leu
20

<210> SEQ ID NO 167
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Solute Carrier Family 28
(sodium-coupled nucleoside transporter), member 2"

<400> SEQUENCE: 167

Glu Leu Met Glu Lys Glu Val Glu Pro Glu Gly Ser Lys Arg Thr Asp

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1 5 10 15

<210> SEQ ID NO 168
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Solute Carrier Family 28 (sodium-coupled nucleoside transporter), member 2"

<400> SEQUENCE: 168

Lys Ala Arg Ser Phe Cys Lys Thr His Ala Arg Leu Phe Lys Lys
1 5 10 15

<210> SEQ ID NO 169
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Solute Carrier Family 28 (sodium-coupled nucleoside transporter), member 2

<400> SEQUENCE: 169

Lys Asn Lys Arg Leu Ser Gly Met Glu Glu Trp Ile Glu Gly Glu Lys
1 5 10 15

<210> SEQ ID NO 170
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Hepatic angiopoietin-related protein

<400> SEQUENCE: 170

Glu Gly Ser Thr Asp Leu Pro Leu Ala Pro Glu Ser Arg Val Asp Pro
1 5 10 15

Glu

<210> SEQ ID NO 171
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Hepatic angiopoietin-related protein

<400> SEQUENCE: 171

Lys Val Ala Gln Gln Gln Arg His Leu Glu Lys Gln His Leu Arg
1 5 10 15

<210> SEQ ID NO 172
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Hepatic angiopoietin-related protein

<400> SEQUENCE: 172

Asp His Lys His Leu Asp His Glu Val Ala Lys Pro Ala Arg Arg Lys
1 5 10 15

Arg Leu Pro Glu
20

<210> SEQ ID NO 173
<211> LENGTH: 17

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Carcinoembryonic antigen-related cell adhesion molecule 5

<400> SEQUENCE: 173

Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly Lys Glu
1 5 10 15

Cys

<210> SEQ ID NO 174
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Carcinoembryonic antigen-related cell adhesion molecule 5

<400> SEQUENCE: 174

Lys Ser Asp Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr
1 5 10 15

Pro Glu Leu Pro Lys
20

<210> SEQ ID NO 175
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Carcinoembryonic antigen-related cell adhesion molecule 5

<400> SEQUENCE: 175

Lys Pro Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu
1 5 10 15

Ala Gln

<210> SEQ ID NO 176
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from podocalyxin-like protein 1

<400> SEQUENCE: 176

Asp Glu Lys Leu Ile Ser Leu Ile Cys Arg Ala Val Lys Ala Thr Phe
1 5 10 15

Asn Pro Ala Gln Asp Lys
20

<210> SEQ ID NO 177
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from podocalyxin-like protein 1

<400> SEQUENCE: 177

Lys Asp Lys Trp Asp Glu Leu Lys Glu Ala Gly Val Ser Asp Met Lys
1 5 10 15

Leu Gly Asp

<210> SEQ ID NO 178
<211> LENGTH: 23

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from podocalyxin-like protein 1

<400> SEQUENCE: 178

Asp Ser Trp Ile Val Pro Leu Asp Asn Leu Thr Lys Asp Asp Leu Asp
1 5 10 15

Glu Glu Glu Asp Thr His Leu
20

<210> SEQ ID NO 179
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from glycyl-tRNA synthetase

<400> SEQUENCE: 179

Arg Lys Arg Val Leu Glu Ala Lys Glu Leu Ala Leu Gln Pro Lys Asp
1 5 10 15

Asp Ile Val Asp
20

<210> SEQ ID NO 180
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from glycyl-tRNA synthetase

<400> SEQUENCE: 180

Arg His Gly Val Ser His Lys Val Asp Asp Ser Ser Gly Ser Ile Gly
1 5 10 15

Arg Arg Tyr Ala Arg
20

<210> SEQ ID NO 181
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from glycyl-tRNA synthetase

<400> SEQUENCE: 181

Glu Ala Arg Tyr Pro Leu Phe Glu Gly Gln Glu Thr Gly Lys Lys Glu
1 5 10 15

Thr Ile Glu Glu
20

<210> SEQ ID NO 182
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from LBP protein 32

<400> SEQUENCE: 182

Glu Ala Leu Tyr Pro Gln Arg Arg Ser Tyr Thr Ser Glu Asp Glu Ala
1 5 10 15

Trp Lys

<210> SEQ ID NO 183
<211> LENGTH: 19
<212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from LBP protein 32

<400> SEQUENCE: 183

Asp Tyr Tyr Lys Val Pro Arg Glu Arg Arg Ser Ser Thr Ala Lys Pro
1 5 10 15

Glu Val Glu

<210> SEQ ID NO 184
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from LBP protein 32

<400> SEQUENCE: 184

Asp Lys Tyr Asp Val Pro His Asp Lys Ile Gly Lys Ile Phe Lys Lys
1 5 10 15

Cys Lys Lys

<210> SEQ ID NO 185
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Putative Integral Membrane Transporter (LC27)

<400> SEQUENCE: 185

Asp Pro Asp Gln Tyr Asn Phe Ser Ser Ser Glu Leu Gly Gly Asp Phe
1 5 10 15

Glu Phe Met Asp Asp
20

<210> SEQ ID NO 186
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Putative Integral Membrane Transporter (LC27)

<400> SEQUENCE: 186

Glu Tyr Ile Arg Gln Leu Pro Pro Asn Phe Pro Tyr Arg Asp Asp
1 5 10 15

<210> SEQ ID NO 187
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Putative Integral Membrane Transporter (LC27)

<400> SEQUENCE: 187

Asp Thr Thr Val Leu Leu Pro Pro Tyr Asp Asp Ala Thr Val Asn Gly
1 5 10 15

Ala Ala Lys Glu
20

<210> SEQ ID NO 188
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Peptide from Cyclin E2

<400> SEQUENCE: 188

Arg Arg Glu Glu Val Thr Lys Lys His Gln Tyr Glu Ile Arg
1 5 10

<210> SEQ ID NO 189
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Cyclin E2

<400> SEQUENCE: 189

Lys Glu Ser Arg Tyr Val His Asp Lys His Phe Glu Val Leu His Ser
1 5 10 15

Asp Leu Glu

<210> SEQ ID NO 190
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Cyclin E2

<400> SEQUENCE: 190

Asp Phe Phe Asp Arg Phe Met Leu Thr Gln Lys Asp Ile Asn Lys
1 5 10 15

<210> SEQ ID NO 191
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from KIAA0253

<400> SEQUENCE: 191

Glu Ser Lys His Phe Thr Arg Asp Leu Met Glu Lys Leu Lys Gly Arg
1 5 10 15

Thr Ser Arg

<210> SEQ ID NO 192
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from KIAA0253

<400> SEQUENCE: 192

Glu Thr Asp Arg Leu Pro Arg Cys Val Arg Ser Thr Ala Arg Leu Ala
1 5 10 15

Arg

<210> SEQ ID NO 193
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from KIAA0253

<400> SEQUENCE: 193

Glu Ser Arg Trp Lys Asp Ile Arg Ala Arg Ile Phe Leu Ile Ala Ser
1 5 10 15

Lys Glu Leu Glu
20

-continued

<210> SEQ ID NO 194
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from FXYD domain-containing ion transport regulator 3

<400> SEQUENCE: 194

Ser Glu Trp Arg Ser Ser Gly Glu Gln Ala Gly Arg
1 5 10

<210> SEQ ID NO 195
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from FXYD domain-containing ion transport regulator 3

<400> SEQUENCE: 195

Lys Cys Lys Cys Lys Phe Gly Gln Lys Ser Gly His His Pro Gly Glu
1 5 10 15

<210> SEQ ID NO 196
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from FXYD domain-containing ion transport regulator 3

<400> SEQUENCE: 196

Lys Val Thr Leu Gly Leu Leu Val Phe Leu Ala Gly Phe Pro Val Leu
1 5 10 15

Asp Ala Asn Asp Leu Glu Asp
20

<210> SEQ ID NO 197
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Immunoglobulin Superfamily, Member 3

<400> SEQUENCE: 197

Lys Val Ala Lys Glu Ser Asp Ser Val Phe Val Leu Lys Ile Tyr His
1 5 10 15

Leu Arg Gln Glu Asp
20

<210> SEQ ID NO 198
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Immunoglobulin Superfamily, Member 3

<400> SEQUENCE: 198

Glu Arg Glu Lys Thr Val Thr Gly Glu Phe Ile Asp Lys Glu Ser Lys
1 5 10 15

Arg Pro Lys

-continued

<210> SEQ ID NO 199
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Immunoglobulin Superfamily, Member 3

<400> SEQUENCE: 199

Lys Arg Ala Glu Asp Thr Ala Gly Gln Thr Ala Leu Thr Val Met Arg
1 5 10 15

Pro Asp

<210> SEQ ID NO 200
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from STAM2

<400> SEQUENCE: 200

Lys Val Ala Arg Lys Val Arg Ala Leu Tyr Asp Phe Glu Ala Val Glu
1 5 10 15

Asp Asn Glu

<210> SEQ ID NO 201
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from STAM2

<400> SEQUENCE: 201

Glu Thr Glu Val Ala Ala Val Asp Lys Leu Asn Val Ile Asp Asp Asp
1 5 10 15

Val Glu

<210> SEQ ID NO 202
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from STAM2

<400> SEQUENCE: 202

Glu Ile Lys Lys Ser Glu Pro Glu Pro Val Tyr Ile Asp Glu Asp Lys
1 5 10 15

Met Asp Arg

<210> SEQ ID NO 203
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Dickkopf Homolog 1

<400> SEQUENCE: 203

Asp Glu Glu Cys Gly Thr Asp Glu Tyr Cys Ala Ser Pro Thr Arg Gly
1 5 10 15

Gly Asp

<210> SEQ ID NO 204
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Dickkopf Homolog 1

<400> SEQUENCE: 204

Arg Gly Glu Ile Glu Glu Thr Ile Thr Glu Ser Phe Gly Asn Asp His
1 5 10 15

Ser Thr Leu Asp
20

<210> SEQ ID NO 205
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Putative Anion Transporter 1

<400> SEQUENCE: 205

Met Asp Leu Arg Arg Arg Asp Tyr His Met Glu Arg Pro Leu Leu Asn
1 5 10 15

Gln Glu His Leu Glu Glu
20

<210> SEQ ID NO 206
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Putative Anion Transporter 1

<400> SEQUENCE: 206

Asp Thr Asp Ile Tyr Arg Asp Val Ala Glu Tyr Ser Glu Ala Lys Glu
1 5 10 15

<210> SEQ ID NO 207
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Putative Anion Transporter 1

<400> SEQUENCE: 207

Glu Phe Tyr Ser Asp Ala Leu Lys Gln Arg Cys Gly Val Asp Val Asp
1 5 10 15

Phe Leu Ile Ser Gln Lys Lys Lys
20

<210> SEQ ID NO 208
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Wnt Inhibitory Factor 1

<400> SEQUENCE: 208

Asp Ala His Gln Ala Arg Val Leu Ile Gly Phe Glu Glu Asp Ile Leu
1 5 10 15

Ile Val Ser Glu
20

<210> SEQ ID NO 209
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Wnt Inhibitory Factor 1

-continued

<400> SEQUENCE: 209

Glu Arg Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His Cys
1 5 10 15

Glu Lys

<210> SEQ ID NO 210
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from PRAME

<400> SEQUENCE: 210

Asp Ile Lys Met Ile Leu Lys Met Val Gln Leu Asp Ser Ile Glu Asp
1 5 10 15

Leu Glu

<210> SEQ ID NO 211
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from PRAME

<400> SEQUENCE: 211

Lys Arg Lys Val Asp Gly Leu Ser Thr Glu Ala Glu Gln Pro Phe Ile
1 5 10 15

Pro Val Glu

<210> SEQ ID NO 212
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from PRAME

<400> SEQUENCE: 212

Lys Glu Gly Ala Cys Asp Glu Leu Phe Ser Tyr Leu Ile Glu Lys Val
1 5 10 15

Lys Arg Lys Lys
20

<210> SEQ ID NO 213
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Prostaglandin E Synthase

<400> SEQUENCE: 213

Arg Leu Arg Lys Lys Ala Phe Ala Asn Pro Glu Asp Ala Leu Arg
1 5 10 15

<210> SEQ ID NO 214
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Prostaglandin E Synthase

<400> SEQUENCE: 214

Arg Ser Asp Pro Asp Val Glu Arg Cys Leu Arg Ala His Arg Asn Asp
1 5 10 15

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<210> SEQ ID NO 215
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Prostaglandin E Synthase

<400> SEQUENCE: 215

Arg Val Ala His Thr Val Ala Tyr Leu Gly Lys Leu Arg Ala Pro Ile
1 5 10 15

Arg

<210> SEQ ID NO 216
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Solute Carrier Family 7, member 5/LAT1 protein

<400> SEQUENCE: 216

Lys Arg Arg Ala Leu Ala Ala Pro Ala Ala Glu Glu Lys Glu Glu Ala
1 5 10 15

Arg

<210> SEQ ID NO 217
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Solute Carrier Family 7, member 5/LAT1 protein

<400> SEQUENCE: 217

Glu Ala Arg Glu Lys Met Leu Ala Ala Lys Ser Ala Asp Gly Ser Ala
1 5 10 15

Pro Ala Gly Glu
20

<210> SEQ ID NO 218
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Solute Carrier Family 7, member 5/LAT1 protein

<400> SEQUENCE: 218

Met Ile Trp Leu Arg His Arg Lys Pro Glu Leu Glu Arg Pro Ile Lys
1 5 10 15

<210> SEQ ID NO 219
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from v-maf musculoaponeurotic fibrosarcoma (avian) oncogene family, protein K or NF-E2p18"

<400> SEQUENCE: 219

Lys Pro Asn Lys Ala Leu Lys Val Lys Lys Glu Ala Gly Glu
1 5 10

<210> SEQ ID NO 220
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Peptide from v-maf musculoaponeurotic fibrosarcoma (avian) oncogene family, protein K or NF-E2p18"

<400> SEQUENCE: 220

Lys Arg Val Thr Gln Lys Glu Glu Leu Glu Arg Gln Arg Val Glu Leu
1 5 10 15

Gln Gln Glu Val Glu Lys
20

<210> SEQ ID NO 221
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from v-maf musculoaponeurotic fibrosarcoma (avian) oncogene family, protein K or NF-E2p18"

<400> SEQUENCE: 221

Arg Leu Glu Leu Asp Ala Leu Arg Ser Lys Tyr Glu
1 5 10

<210> SEQ ID NO 222
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from CEGP1

<400> SEQUENCE: 222

Lys Met His Thr Asp Gly Arg Ser Cys Leu Glu Arg Glu Asp Thr Val
1 5 10 15

Leu Glu Val Thr Glu
20

<210> SEQ ID NO 223
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from CEGP1

<400> SEQUENCE: 223

Lys Lys Gly Phe Lys Leu Leu Thr Asp Glu Lys Ser Cys Gln Asp Val
1 5 10 15

Asp Glu

<210> SEQ ID NO 224
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from CEGP1

<400> SEQUENCE: 224

Lys Arg Thr Glu Lys Arg Leu Arg Lys Ala Ile Arg Thr Leu Arg Lys
1 5 10 15

Ala Val His Arg Glu
20

<210> SEQ ID NO 225
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from GABRE gamma-aminobutyric acid

-continued

(GABA) A receptor, epsilon

<400> SEQUENCE: 225

Arg Val Glu Gly Pro Gln Thr Glu Ser Lys Asn Glu Ala Ser Ser Arg
1 5 10 15

Asp

<210> SEQ ID NO 226
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from GABRE gamma-aminobutyric acid
(GABA) A receptor, epsilon

<400> SEQUENCE: 226

Glu Glu Thr Lys Ser Thr Glu Thr Glu Thr Gly Ser Arg Val Gly Lys
1 5 10 15

Leu Pro Glu

<210> SEQ ID NO 227
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from S100 calcium-binding protein A10

<400> SEQUENCE: 227

Asp Lys Gly Tyr Leu Thr Lys Glu Asp Leu Arg Val Leu Met Glu Lys
1 5 10 15

Glu

<210> SEQ ID NO 228
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from S100 calcium-binding protein A10

<400> SEQUENCE: 228

Lys Asp Pro Leu Ala Val Asp Lys Ile Met Lys Asp Leu Asp Gln Cys
1 5 10 15

Arg Asp Gly Lys
20

<210> SEQ ID NO 229
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from v-myb avian myeloblastosis viral
oncogene homolog-like 2

<400> SEQUENCE: 229

Glu Glu Asp Leu Lys Glu Val Leu Arg Ser Glu Ala Gly Ile Glu Leu
1 5 10 15

Ile Ile Glu Asp Asp Ile Arg
20

<210> SEQ ID NO 230
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from v-myb avian myeloblastosis viral

-continued

oncogene homolog-like 2

<400> SEQUENCE: 230

Met Ser Arg Arg Thr Arg Cys Glu Asp Leu Asp Glu Leu His Tyr Gln
1 5 10 15

Asp Thr Asp Ser Asp
20

<210> SEQ ID NO 231
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from v-myb avian myeloblastosis viral oncogene homolog-like 2

<400> SEQUENCE: 231

Arg Arg Ser Pro Ile Lys Lys Val Arg Lys Ser Leu Ala Leu Asp Ile
1 5 10 15

Val Asp Glu Asp
20

<210> SEQ ID NO 232
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from nucleoside phosphorylase

<400> SEQUENCE: 232

Glu Asp Tyr Lys Asn Thr Ala Glu Trp Leu Leu Ser His Thr Lys His
1 5 10 15

Arg

<210> SEQ ID NO 233
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from nucleoside phosphorylase

<400> SEQUENCE: 233

Asp Glu Arg Phe Gly Asp Arg Phe Pro Ala Met Ser Asp Ala Tyr Asp
1 5 10 15

Arg Thr Met Arg Gln Arg
20

<210> SEQ ID NO 234
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from nucleoside phosphorylase

<400> SEQUENCE: 234

Lys Val Ile Met Asp Tyr Glu Ser Leu Glu Lys Ala Asn His Glu Glu
1 5 10 15

<210> SEQ ID NO 235
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from aldo-keto reductase family 1, member C4

-continued

<400> SEQUENCE: 235

Asp Gln Asp Arg Lys Ser Arg Leu Met Gly Leu Glu Ala Leu Lys Ser
1 5 10 15

His Ile Met Ala Ala Lys
20

<210> SEQ ID NO 236
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from aldo-keto reductase family 1, member C4

<400> SEQUENCE: 236

Lys Gly Val Ile Val Asp Lys Asp Phe Ser His Pro Gln Met Pro Lys
1 5 10 15

Lys Val Glu Asp
20

<210> SEQ ID NO 237
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from aldo-keto reductase family 1, member C4

<400> SEQUENCE: 237

Arg Met Ile Leu Lys Ile Asp Asp Ile Arg Lys Pro Gly Glu Ser Glu
1 5 10 15

Glu

<210> SEQ ID NO 238
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Non-metastatic cells 1, protein (NM23A)

<400> SEQUENCE: 238

Arg Leu Gln Pro Glu Phe Lys Pro Lys Gln Leu Glu Gly Thr Met Ala
1 5 10 15

Asn Cys Glu Arg
20

<210> SEQ ID NO 239
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Non-metastatic cells 1, protein (NM23A)

<400> SEQUENCE: 239

Lys Phe Met Gln Ala Ser Glu Asp Leu Leu Lys Glu His Tyr Val Asp
1 5 10 15

Leu Lys Asp Arg
20

<210> SEQ ID NO 240
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Non-metastatic cells 1, protein
(NM23A)

<400> SEQUENCE: 240

Asp Ser Val Glu Ser Ala Glu Lys Glu Ile Gly Leu Trp Phe His Pro
1 5 10 15

Glu Glu Leu Val Asp
20

<210> SEQ ID NO 241
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Squalene epoxidase

<400> SEQUENCE: 241

Lys Ser Pro Pro Glu Ser Glu Asn Lys Glu Gln Leu Glu Ala Arg Arg
1 5 10 15

Arg Arg

<210> SEQ ID NO 242
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Squalene epoxidase

<400> SEQUENCE: 242

Arg Asp Gly Arg Lys Val Thr Val Ile Glu Arg Asp Leu Lys Glu Pro
1 5 10 15

Asp Arg

<210> SEQ ID NO 243
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Squalene epoxidase

<400> SEQUENCE: 243

Asp His Leu Lys Glu Pro Phe Leu Glu Ala Thr Asp Asn Ser His Leu
1 5 10 15

Arg

<210> SEQ ID NO 244
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Pregnancy-induced growth inhibitor

<400> SEQUENCE: 244

Asp Leu Glu Val Lys Asp Trp Met Gln Lys Lys Arg Arg Gly Leu Arg
1 5 10 15

Asn Ser Arg

<210> SEQ ID NO 245
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Pregnancy-induced growth inhibitor

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<400> SEQUENCE: 245

Glu Tyr His Lys Val His Gln Met Met Arg Glu Gln Ser Ile Leu Ser
1 5 10 15

Pro Ser Pro Tyr Glu Gly Tyr Arg
20

<210> SEQ ID NO 246
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Pregnancy-induced growth inhibitor

<400> SEQUENCE: 246

Arg His Gln Leu Leu Cys Phe Lys Glu Asp Cys Gln Ala Val Phe Gln
1 5 10 15

Asp Leu Glu Gly Val Glu Lys
20

<210> SEQ ID NO 247
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Putative 4TM Mal-like protein

<400> SEQUENCE: 247

Gly Pro Asp Ile Leu Arg Thr Tyr Ser Gly Ala Phe Val Cys Leu Glu
1 5 10 15

<210> SEQ ID NO 248
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Putative 4TM Mal-like protein

<400> SEQUENCE: 248

Cys Ser Leu Gly Leu Ala Leu Arg Arg Trp Arg Pro
1 5 10

<210> SEQ ID NO 249
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from aldo-keto reductase family 1,
member C1/C2

<400> SEQUENCE: 249

Arg Tyr Leu Thr Leu Asp Ile Phe Ala Gly Pro Pro Asn Tyr Pro Phe
1 5 10 15

Ser Asp Glu Tyr
20

<210> SEQ ID NO 250
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from aldo-keto reductase family 1,
member C4

<400> SEQUENCE: 250

His Tyr Phe Asn Ser Asp Ser Phe Ala Ser His Pro Asn Tyr Pro Tyr
1 5 10 15

-continued

Ser Asp Glu Tyr
20

<210> SEQ ID NO 251
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from aldo-keto reductase family 1, member C4

<400> SEQUENCE: 251

Arg Tyr Val Val Met Asp Phe Leu Met Asp His Pro Asp Tyr Pro Phe
1 5 10 15

Ser Asp Glu Tyr
20

<210> SEQ ID NO 252
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Putative ParB-like nuclease domain containing protein

<400> SEQUENCE: 252

Asp Pro Ala Lys Val Gln Ser Leu Val Asp Thr Ile Arg Glu Asp Pro
1 5 10 15

Asp

<210> SEQ ID NO 253
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Putative ParB-like nuclease domain containing protein

<400> SEQUENCE: 253

Arg Glu Thr Ile Pro Ala Lys Leu Val Gln Ser Thr Leu Ser Asp Leu
1 5 10 15

Arg

<210> SEQ ID NO 254
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Putative glucose transporter-like protein

<400> SEQUENCE: 254

Ser Asp Thr Thr Glu Glu Leu Thr Val Ile Lys Ser Ser Leu Lys Asp
1 5 10 15

Glu

<210> SEQ ID NO 255
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Putative glucose transporter-like protein

<400> SEQUENCE: 255

-continued

His Ser Arg Ser Ser Leu Met Pro Leu Arg Asn Asp Val Asp Lys Arg
1 5 10 15

<210> SEQ ID NO 256
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from CLIC5

<400> SEQUENCE: 256

Asp Ala Asn Thr Cys Gly Glu Asp Lys Gly Ser Arg Arg Lys Phe Leu
1 5 10 15

Asp Gly Asp Glu
20

<210> SEQ ID NO 257
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from AX119005

<400> SEQUENCE: 257

Gln Leu Glu Glu Met Thr Glu Leu Glu Ser Pro Lys Cys Lys Arg Gln
1 5 10 15

Glu Asn Glu Gln
20

<210> SEQ ID NO 258
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from FARP1

<400> SEQUENCE: 258

Gln Ala Asp Gly Ala Ala Ser Ala Pro Thr Glu Glu Glu Glu Glu Val
1 5 10 15

Val Lys Asp Arg
20

<210> SEQ ID NO 259
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from TRPS1

<400> SEQUENCE: 259

Ser Gly Asp Ser Leu Glu Thr Lys Glu Asp Gln Lys Met Ser Pro Lys
1 5 10 15

Ala Thr Glu Glu
20

<210> SEQ ID NO 260
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from FAT

<400> SEQUENCE: 260

Lys Ile Arg Leu Pro Glu Arg Glu Lys Pro Asp Arg Glu Arg Asn Ala
1 5 10 15

-continued

Arg Arg Glu Pro
20

<210> SEQ ID NO 261
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from GRN

<400> SEQUENCE: 261

Arg Gly Thr Lys Cys Leu Arg Arg Glu Ala Pro Arg Trp Asp Ala Pro
1 5 10 15

Leu Arg Asp Pro
20

<210> SEQ ID NO 262
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from NDRG1

<400> SEQUENCE: 262

Gly Thr Arg Ser Arg Ser His Thr Ser Glu Gly Thr Arg Ser Arg Ser
1 5 10 15

His Thr Ser Glu
20

<210> SEQ ID NO 263
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from FABP5

<400> SEQUENCE: 263

Glu Glu Thr Thr Ala Asp Gly Arg Lys Thr Gln Thr Val Cys Asn Phe
1 5 10 15

Thr Asp

<210> SEQ ID NO 264
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from CDKN1C

<400> SEQUENCE: 264

Ala Lys Arg Lys Arg Ser Ala Pro Glu Lys Ser Ser Gly Asp Val Pro
1 5 10 15

<210> SEQ ID NO 265
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from AMACR

<400> SEQUENCE: 265

Arg Val Asp Arg Pro Gly Ser Arg Tyr Asp Val Ser Arg Leu Gly Arg
1 5 10 15

Gly Lys Arg Ser
20

-continued

<210> SEQ ID NO 266
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from GABRB3

<400> SEQUENCE: 266

Glu Thr Val Asp Lys Leu Leu Lys Gly Tyr Asp Ile Arg Leu Arg Pro
1 5 10 15

Asp

<210> SEQ ID NO 267
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from KIAA0872 protein

<400> SEQUENCE: 267

Ala Pro Gly Gly Ala Glu Asp Leu Glu Asp Thr Gln Phe Pro Ser Glu
1 5 10 15

Glu Ala Arg Glu
20

<210> SEQ ID NO 268
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from TNFRSF21

<400> SEQUENCE: 268

Arg Lys Ser Ser Arg Thr Leu Lys Lys Gly Pro Arg Gln Asp Pro Ser
1 5 10 15

Ala Ile Val Glu
20

<210> SEQ ID NO 269
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from TRIP8

<400> SEQUENCE: 269

Gly Ser Glu Ser Gly Asp Ser Asp Glu Ser Glu Ser Lys Ser Glu Gln
1 5 10 15

Arg Thr Lys Arg
20

<210> SEQ ID NO 270
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from BSTP5

<400> SEQUENCE: 270

Glu Ala Asp Ser Gly Asp Ala Arg Arg Leu Pro Arg Ala Arg Gly Glu
1 5 10 15

Arg Arg Arg His
20

<210> SEQ ID NO 271

-continued

<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from cdc25b

<400> SEQUENCE: 271

Arg Leu Glu Arg Pro Gln Asp Arg Asp Thr Pro Val Gln Asn Lys Arg
1 5 10 15

Arg Arg Ser

<210> SEQ ID NO 272
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from laminin, beta 1 (lamb1)

<400> SEQUENCE: 272

Asp Arg Val Glu Asp Val Met Met Glu Arg Glu Ser Gln Phe Lys Glu
1 5 10 15

Lys Gln Glu

<210> SEQ ID NO 273
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from papillary renal cell carcinoma
(translocation-associated) (prcc)

<400> SEQUENCE: 273

Asp Glu Ala Phe Lys Arg Leu Gln Gly Lys Arg Asn Arg Gly Arg Glu
1 5 10 15

Glu

<210> SEQ ID NO 274
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from TNFSF10

<400> SEQUENCE: 274

Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln
1 5 10 15

<210> SEQ ID NO 275
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from titin

<400> SEQUENCE: 275

Lys Arg Asp Lys Glu Gly Val Arg Trp Thr Lys Cys Asn Lys Lys Thr
1 5 10 15

Leu Thr Asp

<210> SEQ ID NO 276
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from DNA fragmentation factor, 45 kD,
alpha polypeptide

-continued

<400> SEQUENCE: 276

Lys Glu Gly Ser Leu Leu Ser Lys Gln Glu Glu Ser Lys Ala Ala Phe
1 5 10 15

Gly Glu Glu

<210> SEQ ID NO 277
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Caspase 2

<400> SEQUENCE: 277

Glu Ser Asp Ala Gly Lys Glu Lys Leu Pro Lys Met Arg Leu Pro Thr
1 5 10 15

Arg Ser Asp

<210> SEQ ID NO 278
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from GSPT1

<400> SEQUENCE: 278

Glu Arg Asp Lys Gly Lys Thr Val Glu Val Gly Arg Ala Tyr Phe Glu
1 5 10 15

Thr Glu Lys

<210> SEQ ID NO 279
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from GCN5L2

<400> SEQUENCE: 279

Glu Lys Phe Arg Val Glu Lys Asp Lys Leu Val Pro Glu Lys Arg
1 5 10 15

<210> SEQ ID NO 280
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from FLJ23293

<400> SEQUENCE: 280

Glu Asn Tyr Glu Asp Asp Asp Leu Val Asn Ser Asp Glu Val Met Lys
1 5 10 15

Lys Pro

<210> SEQ ID NO 281
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from HSPC037 protein

<400> SEQUENCE: 281

Pro Lys Ala Asp Glu Ile Arg Thr Leu Val Lys Asp Met Trp Asp Thr
1 5 10 15

Arg

-continued

<210> SEQ ID NO 282
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from FLJ20093

<400> SEQUENCE: 282

Arg Lys Arg Cys Leu Glu Asp Ser Glu Asp Phe Gly Val Lys Lys Ala
1 5 10 15

Arg Thr Glu

<210> SEQ ID NO 283
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from KIAA0176

<400> SEQUENCE: 283

Glu Pro Lys Ser Phe Leu Cys Arg Leu Cys Cys Gln Glu Asp Pro Glu
1 5 10 15

Leu Asp Ser

<210> SEQ ID NO 284
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from KIAA0856

<400> SEQUENCE: 284

Glu Glu Tyr Asp Arg Glu Ser Lys Ser Ser Asp Asp Val Asp Tyr Arg
1 5 10 15

Gly Ser

<210> SEQ ID NO 285
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from FLJ14642

<400> SEQUENCE: 285

Glu Gln Arg Ala Arg Trp Glu Arg Lys Arg Ala Cys Thr Ala Arg Glu
1 5 10 15

<210> SEQ ID NO 286
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from RNA methyltransferase (HpaII tiny fragments locus 9C)

<400> SEQUENCE: 286

Glu Arg Lys Gln Leu Glu Cys Glu Gln Val Leu Gln Lys Leu Ala Lys
1 5 10 15

Glu

<210> SEQ ID NO 287
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Serine rich hypothetical protein

<400> SEQUENCE: 287

Arg Asn Ser Glu Thr Lys Val Arg Arg Ser Thr Arg Leu Gln Lys Asp
1 5 10 15

Leu Glu Asn

<210> SEQ ID NO 288
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Similar to mitotic phosphoprotein
44 [Xenopus laevis]

<400> SEQUENCE: 288

Ser Asp Tyr Gln Val Ile Ser Asp Arg Gln Thr Pro Lys Lys Asp Glu
1 5 10 15

<210> SEQ ID NO 289
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from SMC4

<400> SEQUENCE: 289

Asp Ile Glu Gly Lys Leu Pro Gln Thr Glu Gln Glu Leu Lys Glu
1 5 10 15

<210> SEQ ID NO 290
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from phosphatidylserine synthase

<400> SEQUENCE: 290

Asp Asp Val Asn Tyr Lys Met His Phe Arg Met Ile Asn Glu Gln Gln
1 5 10 15

Val Glu Asp

<210> SEQ ID NO 291
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from polo (Drosophia)-like kinase

<400> SEQUENCE: 291

Glu Asn Pro Leu Pro Glu Arg Pro Arg Glu Lys Glu Glu Pro Val Val
1 5 10 15

Arg

<210> SEQ ID NO 292
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Pirin

<400> SEQUENCE: 292

Arg Glu Gln Ser Glu Gly Val Gly Ala Arg Val Arg Arg Ser Ile Gly
1 5 10 15

-continued

Arg Pro Glu

<210> SEQ ID NO 293
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from ABCA3

<400> SEQUENCE: 293

Pro Arg Ala Val Ala Gly Lys Glu Glu Glu Asp Ser Asp Pro Glu Lys
1 5 10 15

Ala Leu Arg

<210> SEQ ID NO 294
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from ABCA7

<400> SEQUENCE: 294

Glu Lys Ala Asp Thr Asp Met Glu Gly Ser Val Asp Thr Arg Gln Glu
1 5 10 15

Lys

<210> SEQ ID NO 295
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from ABCB7

<400> SEQUENCE: 295

Arg Val Gln Asn His Asp Asn Pro Lys Trp Glu Ala Lys Lys Glu Asn
1 5 10 15

Ile Ser Lys

<210> SEQ ID NO 296
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from ABCC12

<400> SEQUENCE: 296

Arg Ser Pro Pro Ala Lys Gly Ala Thr Gly Pro Glu Glu Gln Ser Asp
1 5 10 15

Ser Leu Lys

<210> SEQ ID NO 297
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from ABCG2

<400> SEQUENCE: 297

Arg Glu Glu Asp Phe Lys Ala Thr Glu Ile Ile Glu Pro Ser Lys Gln
1 5 10 15

Asp Lys Pro

<210> SEQ ID NO 298
<211> LENGTH: 15

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from SLC21A8

<400> SEQUENCE: 298

Asp Lys Thr Cys Met Lys Trp Ser Thr Asn Ser Cys Gly Ala Gln
1 5 10 15

<210> SEQ ID NO 299
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from SLC22A6

<400> SEQUENCE: 299

Asp Ala Asn Leu Ser Lys Asn Gly Gly Leu Glu Val Trp Leu
1 5 10

<210> SEQ ID NO 300
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from SLC35A2

<400> SEQUENCE: 300

Glu Pro Phe Leu Pro Lys Leu Leu Thr Lys
1 5 10

<210> SEQ ID NO 301
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from cdc25b isoforms 1,3

<400> SEQUENCE: 301

Arg Lys Ser Glu Ala Gly Ser Gly Ala Ala Ser Ser Ser Gly Glu Asp
1 5 10 15

Lys Glu Asn

<210> SEQ ID NO 302
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from SCD stearoyl-CoA desaturase
delta-9-desaturase

<400> SEQUENCE: 302

Asp Asp Ile Tyr Asp Pro Thr Tyr Lys Asp Lys Glu Gly Pro Ser Pro
1 5 10 15

Lys Val Glu

<210> SEQ ID NO 303
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from MAPK12 mitogen-activated protein
kinase 12

<400> SEQUENCE: 303

Gln Ser Asp Glu Ala Lys Asn Asn Met Lys Gly Leu Pro Glu Leu Glu
1 5 10 15

-continued

Lys Lys Asp

<210> SEQ ID NO 304
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from NFKB2 nuclear factor of kappa light 2 (p49/p100)

<400> SEQUENCE: 304

Ser Arg Pro Gln Gly Leu Thr Glu Ala Glu Gln Arg Glu Leu Glu Gln
1 5 10 15

Glu Ala Lys

<210> SEQ ID NO 305
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from TNFRSF5

<400> SEQUENCE: 305

Arg Val Gln Gln Lys Gly Thr Ser Glu Thr Asp Thr Ile Cys
1 5 10

<210> SEQ ID NO 306
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from EBI3 Epstein-Barr virus induced gene 3

<400> SEQUENCE: 306

Val Arg Leu Ser Pro Leu Ala Glu Arg Gln Leu Gln Val Gln Trp Glu
1 5 10 15

<210> SEQ ID NO 307
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from ZNF339

<400> SEQUENCE: 307

Arg Arg Ser Leu Gly Val Ser Val Arg Ser Trp Asp Glu Leu Pro Asp
1 5 10 15

Glu Lys Arg

<210> SEQ ID NO 308
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from DAB2IP

<400> SEQUENCE: 308

Asp Glu Gly Leu Gly Pro Asp Pro Pro His Arg Asp Arg Leu Arg Ser
1 5 10 15

Lys

<210> SEQ ID NO 309
<211> LENGTH: 18
<212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from PPFIA1

<400> SEQUENCE: 309

Ser Gly Lys Arg Ser Ser Asp Gly Ser Leu Ser His Glu Glu Asp Leu
1 5 10 15

Ala Lys

<210> SEQ ID NO 310
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from CAB66760

<400> SEQUENCE: 310

Ser Gln Glu Arg Ser Asp Ser Pro Glu Ile Cys His Tyr Glu Lys Ser
1 5 10 15

Phe His Lys

<210> SEQ ID NO 311
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from novel hypothetical protein

<400> SEQUENCE: 311

Lys Val Asn Pro Glu Pro Thr His Glu Ile Arg Cys Asn Ser Glu Val
1 5 10 15

Lys

<210> SEQ ID NO 312
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from frizzled homolog 7 FZD7

<400> SEQUENCE: 312

Ser Asp Gly Arg Gly Arg Pro Ala Phe Pro Phe Ser Cys Pro Arg Gln
1 5 10 15

<210> SEQ ID NO 313
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from SLC3A2

<400> SEQUENCE: 313

Gly Ser Lys Glu Asp Phe Asp Ser Leu Leu Gln Ser Ala Lys Lys
1 5 10 15

<210> SEQ ID NO 314
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from PLA2R1 phospholipase A2 receptor 1

<400> SEQUENCE: 314

Gln Lys Glu Glu Lys Thr Trp His Glu Ala Leu Arg Ser Cys Gln Ala
1 5 10 15

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Asp Asn

<210> SEQ ID NO 315
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from KIAA0182

<400> SEQUENCE: 315

Glu Lys Ala Glu Glu Gly Pro Arg Lys Arg Glu Pro Ala Pro Leu Asp
1 5 10 15

Lys

<210> SEQ ID NO 316
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from thymidine kinase 2, mitochondrial

<400> SEQUENCE: 316

Glu Gln Asn Arg Asp Arg Ile Leu Thr Pro Glu Asn Arg Lys
1 5 10

<210> SEQ ID NO 317
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from FLJ12799

<400> SEQUENCE: 317

Arg Asp Trp Tyr Ile Gly Leu Val Ser Asp Glu Lys Trp Lys
1 5 10

<210> SEQ ID NO 318
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from KIAA1007

<400> SEQUENCE: 318

Asp Ser Tyr Leu Lys Thr Arg Ser Pro Val Thr Phe Leu Ser Asp Leu
1 5 10 15

Arg

<210> SEQ ID NO 319
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from DKFZP566O1646

<400> SEQUENCE: 319

Lys Cys Arg Gly Glu Thr Val Ala Lys Glu Ile Ser Glu Ala Met Lys
1 5 10 15

Ser

<210> SEQ ID NO 320
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from ART-4

-continued

<400> SEQUENCE: 320

Lys Pro Pro Gln Glu Thr Glu Lys Gly His Ser Ala Cys Glu Pro Glu
1 5 10 15

Asn

<210> SEQ ID NO 321
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from GNA12

<400> SEQUENCE: 321

Glu Arg Arg Ala Gly Ser Gly Ala Arg Asp Ala Glu Arg Glu
1 5 10

<210> SEQ ID NO 322
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from GrpE-like protein cochaperone
(HMGE)

<400> SEQUENCE: 322

Ser Glu Gln Lys Ala Asp Pro Pro Ala Thr Glu Lys Thr Leu Leu Glu
1 5 10 15

<210> SEQ ID NO 323
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from FLJ34922

<400> SEQUENCE: 323

Glu Ala Glu Trp Ser Gln Gly Val Gln Gly Thr Leu Arg Ile Lys Lys
1 5 10 15

Tyr Leu Thr

<210> SEQ ID NO 324
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from FLJ20457

<400> SEQUENCE: 324

Glu Glu Ser Lys Ser Ile Thr Glu Gly Leu Leu Thr Gln Lys Gln Tyr
1 5 10 15

Glu

<210> SEQ ID NO 325
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from solute carrier family 7, (cationic
amino acid transporter, y+ system) member 11

<400> SEQUENCE: 325

Gln Asn Phe Lys Asp Ala Phe Ser Gly Arg Asp Ser Ser Ile Thr Arg
1 5 10 15

-continued

<210> SEQ ID NO 326
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Integrin, beta 4

<400> SEQUENCE: 326

Thr Glu Asp Val Asp Glu Phe Arg Asn Lys Leu Gln Gly Glu Arg
1 5 10 15

<210> SEQ ID NO 327
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide from Solute Carrier Family 7, member 5/LAT1 protein

<400> SEQUENCE: 327

Lys Gly Asp Val Ser Asn Leu Asp Pro Asn Phe Ser Phe Glu Gly Thr
1 5 10 15

Lys Leu Asp Val
20

We claim:

1. A kit comprising a prognostic panel of antibodies that includes:

a first antibody that binds to SLC7A5;

a second antibody that binds to HTF9C;

a third antibody that binds to p53;

a fourth antibody that binds to NDRG1; and

a fifth antibody that binds to CEACAM5,

wherein the total number of antibodies included in the kit does not exceed 10.

2. The kit of claim **1**, wherein the kit is for prognosis of a breast cancer patient.

3. The kit of claim **2**, wherein the breast cancer is estrogen receptor positive (ER+).

4. The kit of claim **3**, wherein the breast cancer is node negative (Node −).

5. The kit of claim **2**, wherein across a population of breast cancer patients, a higher level of binding of each of the antibodies correlates with a higher likelihood that the patient will die from breast cancer or have a recurrence.

6. A kit consisting essentially of a prognostic panel of antibodies, the prognostic panel of antibodies including:

a first antibody that binds to SLC7A5;

a second antibody that binds to HTF9C;

a third antibody that binds to p53;

a fourth antibody that binds to NDRG1; and

a fifth antibody that binds to CEACAM5,

wherein the total number of antibodies included in the kit does not exceed 10.

7. The kit of claim **6**, wherein the kit is for prognosis of a breast cancer patient.

8. The kit of claim **7**, wherein the breast cancer is estrogen receptor positive (ER+).

9. The kit of claim **8**, wherein the breast cancer is node negative (Node−).

10. The kit of claim **7**, wherein across a population of breast cancer patients, a higher level of binding of each of the antibodies correlates with a higher likelihood that the patient will die from breast cancer or have a recurrence.

11. A kit comprising a prognostic panel of antibodies, the prognostic panel of antibodies consisting of:

a first antibody that binds to SLC7A5;

a second antibody that binds to HTF9C;

a third antibody that binds to p53;

a fourth antibody that binds to NDRG1; and

a fifth antibody that binds to CEACAM5,

wherein the total number of antibodies included in the kit does not exceed 5.

12. The kit of claim **11**, wherein the kit is for prognosis of a breast cancer patient.

13. The kit of claim **12**, wherein the breast cancer is estrogen receptor positive (ER+).

14. The kit of claim **13**, wherein the breast cancer is node negative (Node−).

15. The kit of claim **12**, wherein across a population of breast cancer patients, a higher level of binding of each of the antibodies correlates with a higher likelihood that the patient will die from breast cancer or have a recurrence.

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